

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:25 ; Search time 411.58 Seconds
(without alignments)
4.500 Million cell updates/sec

Title: US-09-724-406-24

Perfect score: 90

Sequence: 1 DPPYGNPHYVAMDY 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	53.3	470	10 Q9M301	Q9M301 arabidopsis
2	46	51.1	343	2 Q9KJN9	Q9KJN9 myxococcus
3	46	51.1	919	4 Q9NOS7	Q9NOS7 homo sapien
4	45	50.0	761	3 Q9HF59	Q9HF59 ashbya goss
5	44	48.9	527	13 Q9DGB4	Q9DGB4 xenopus lae
6	43.5	48.3	2573	5 Q9G185	Q9G185 plasmodium
7	43	47.8	276	4 Q9NWA9	Q9NWA9 homo sapien
8	43	47.8	329	1 Q58076	Q58076 pyrococcus
9	43	47.8	381	10 Q41556	Q41556 triticum ae
10	43	47.8	484	4 Q9H7L0	Q9H7L0 homo sapien
11	43	47.8	614	4 Q9NW41	Q9NW41 homo sapien
12	43	47.8	855	4 Q9NYK9	Q9NYK9 homo sapien
13	43	47.8	878	4 Q9UFU7	Q9UFU7 homo sapien
14	43	47.8	938	11 Q9JL72	Q9JL72 mus musculus
15	43	47.8	1080	2 Q84688	Q84688 chlamydia t
16	43	47.8	2809	5 Q61230	Q61230 lytechinus
17	42	46.7	497	2 Q9KBN0	Q9KBN0 bacillus ha
18	42	46.7	553	5 Q9GR06	Q9GR06 leishmania
19	42	46.7	860	2 Q9L428	Q9L428 alcaligenes

20	42	46.7	903	6 Q9GLY5	Q9GLY5 oryctolagus
21	42	46.7	973	2 Q86728	Q86728 streptomyce
22	41.5	46.1	363	2 Q9PIS1	Q9PIS1 campylobact
23	41	45.6	26	10 Q9S8A1	Q9S8A1 pinus monti
24	41	45.6	127	5 Q17467	Q17467 schistosoma
25	41	45.6	155	2 Q33696	Q33696 streptococc
26	41	45.6	218	2 Q82505	Q82505 streptomyce
27	41	45.6	222	2 Q9S2D6	Q9S2D6 streptomyce
28	41	45.6	261	2 Q9K6A4	Q9K6A4 bacillus ha
29	41	45.6	357	7 Q30220	Q30220 ateles belz
30	41	45.6	359	4 Q06416	Q06416 homo sapien
31	41	45.6	612	8 Q9TFD0	Q9TFD0 paralichthy
32	41	45.6	950	5 Q20733	Q20733 caenorhabdi
33	41	45.6	973	10 Q9S9Q8	Q9S9Q8 arabidopsis
34	41	45.6	1194	5 Q9W485	Q9W485 drosophila
35	41	45.6	1413	5 Q9VK08	Q9VK08 drosophila
36	41	45.6	1590	2 Q55263	Q55263 streptococc
37	41	45.6	1590	2 Q59983	Q59983 streptococc
38	41	45.6	2197	5 Q96296	Q96296 plasmodium
39	41	45.6	2379	4 Q9Y493	Q9Y493 homo sapien
40	41	45.6	2710	5 Q9XZB8	Q9XZB8 plasmodium
41	40.5	45.0	407	10 Q82036	Q82036 petroselinu
42	40.5	45.0	420	10 Q82037	Q82037 petroselinu
43	40	44.4	171	1 Q59551	Q59551 pyrococcus
44	40	44.4	204	10 Q38895	Q38895 arabidopsis
45	40	44.4	246	10 Q9SV94	Q9SV94 arabidopsis

ALIGNMENTS

RESULT 1

Q9M301 ID Q9M301 PRELIMINARY: PRT; 470 AA.
AC Q9M301;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE HYPOTHETICAL 53.2 KDA PROTEIN.
GN T21J18_90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Meves H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132963; CAB87910.1; -.
DR InterPro; IPR001675; -.
DR Pfam; PF00777; Glyco-transf_29; 1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 53188 MW; 0D0B8EA4CB52C656 CRC64;

Query Match 53.3%; Score 48; DB 10; Length 470;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNPHYVAMDY 14

DB 83 YGLPYVYLDY 93

RESULT 2

Q9KJN9

ID Q9KJN9 PRELIMINARY; PRT; 343 AA.
 AC Q9KJN9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHEICAL 36.6 KDA PROTEIN.
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DZ2;
 RX MEDLINE=20032045; PubMed=10564511;
 RA Cho K., Zusman D.R.;
 RT "Sporulation timing in Myxococcus xanthus is controlled by the espAB
 RT locus.";
 RL Mol. Microbiol. 34:714-725(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DZ2;
 RA Cho K., Zusman D.R.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF163841; AAF87928.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 343 AA; 36580 MW; 16B89C41B1023979 CRC64;

 Query Match 51.1%; Score 46; DB 2; Length 343;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 PPYGNPHY 10
 Db 281 PPYGEPPY 289

 RESULT 3
 Q9NQS7 PRELIMINARY; PRT; 919 AA.
 ID Q9NQS7;
 AC Q9NQS7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE INNER CENTROMERE PROTEIN INCENP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Adams R.R., Eckley D.M., Mackay A., Earnshaw W.C.;
 RT "Characterization and expression of the human INCENP gene.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF282265; AAF87584.1; -
 SQ SEQUENCE 919 AA; 105536 MW; 8F93024E411087C6 CRC64;

 Query Match 51.1%; Score 46; DB 4; Length 919;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

 QY 2 PPYGNPHYAMD 13
 Db 815 PPQINPNHYGMD 826

 RESULT 4
 Q9HF59 PRELIMINARY; PRT; 761 AA.
 ID Q9HF59;
 AC Q9HF59;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CDC24.
 GN CDC24.
 OS Ashbya gossypii (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Eremotheciaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wendland J., Philippsen P.;
 RT "Hyphal morphogenesis is controlled by multiple Rho-protein modules in
 RT the filamentous ascomycete Ashbya gossypii.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF210626; AAG41244.1; -
 SQ SEQUENCE 761 AA; 86025 MW; C7334F46A06BB334 CRC64;

Query Match 50.0%; Score 45; DB 3; Length 761;
 Best Local Similarity 77.8%; Pred. No. 64;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PYGNPHYA 11
 Db 628 PYGHPHYSA 636

RESULT 5
 Q9DGB4 PRELIMINARY; PRT; 527 AA.
 ID Q9DGB4;
 AC Q9DGB4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE DNA POLYMERASE EPSILON SUBUNIT B.
 GN POLE2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Waga S., Sugino A.;
 RT "Xenopus DNA polymerase epsilon subunit B.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB048257; BAB12726.1; -
 SQ SEQUENCE 527 AA; 59688 MW; CF25EE4FB9C711C7 CRC64;

Query Match 48.9%; Score 44; DB 13; Length 527;
 Best Local Similarity 53.8%; Pred. No. 61;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPYGNPHYAMDY 14
 Db 455 PPVSPVYWAYDY 467

RESULT 6
 Q96185 PRELIMINARY; PRT; 2573 AA.
 ID Q96185;
 AC Q96185;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHEICAL 308.1 KDA PROTEIN.
 GN PFB0460C.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.

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RX MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perle M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
RL EMBL; AE001396; AAC11881.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2573 AA; 308142 MW; 49E0D7E8967066CF CRC64;

Query Match 48.3%; Score 43.5; DB 5; Length 2573;
Best Local Similarity 72.7%; Pred. No. 4.2e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 DP-PYGNPHY 10
||| |
Db 1436 DPEAYNPHY 1446
||| |

RESULT 7
Q9NWA9 PRELIMINARY; PRT; 276 AA.
AC Q9NWA9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 29.6 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Makamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Nimomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001032; BAA91474.1; -.
DR InterPro; IPR000286; -.
DR Pfam; PF00850; Hist_deacetyl1; 1.
DR PRINTS; PR01270; HDASUPER.
SQ SEQUENCE 276 AA; 29622 MW; 8C96C7C5B41CD3A1 CRC64;

Query Match 47.8%; Score 43; DB 4; Length 276;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDPYGNPHY 11
||| |
Db 90 DPPMGDPYLA 100
||| |

RESULT 8
O58076 PRELIMINARY; PRT; 329 AA.
ID O58076
AC O58076
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 37.2 KDA PROTEIN PH0338.
GN PH0338.
OS Pyrococcus horikoshii.

Query Match 47.8%; Score 43; DB 10; Length 381;

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OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
RL EMBL; AP000002; BAA29412.1; -.
DR InterPro; IPR000051; -.
DR InterPro; IPR000241; -.
DR InterPro; IPR002052; -.
DR Pfam; PF01170; UPF0020; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 329 AA; 37237 MW; 21485A787DB28294 CRC64;

Query Match 47.8%; Score 43; DB 1; Length 329;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DDPYGNPHYVMD 13
||| |
Db 255 DDPYGNSTTLPMD 267
||| |

RESULT 9
Q41556 PRELIMINARY; PRT; 381 AA.
ID Q41556
AC Q41556
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSCRIPTION FACTOR HBP-1A.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
OC Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HORSHIRIKOMUGI;
RA Nakayama T.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HORSHIRIKOMUGI;
RX MEDLINE=94193693; PubMed=8144592;
RA Mikami K., Sakamoto A., Iwabuchi M.;
RT "The HBP-1 family of wheat basic/leucine zipper proteins interacts
RT with overlapping cis-acting hexamer motifs of plant histone genes.";
RL J. Biol. Chem. 269:9974-9985(1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE BZIP FAMILY.
DR EMBL; D12920; BAA02304.1; -.
DR Mendel; 15812; Triae; 2979; 15812.
DR InterPro; IPR001871; -.
DR Pfam; PF00170; bZIP; 1.
DR PROSITE; PS00036; BZIP_BASIC; 1.
DR SMART; SM00338; BRLZ; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 381 AA; 40683 MW; 448635628C15651F CRC64;

Query Match 47.8%; Score 43; DB 10; Length 381;

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Query Match 47.8%; Score 43; DB 4; Length 614;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPGYGNPHYYA 11
|||||
DB 428 DPPMGDPPEYLA 438

RESULT 12

Q9NYK9 ID Q9NYK9 PRELIMINARY; PRT; 855 AA.
AC Q9NYK9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HISTONE DEACETYLASE 7.
GN HDAC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CERVICAL CARCINOMA;
RA Li S., Fischle W., Verdin E., Walsh M.J.;
RT "A novel class II HDAC is associated with the transcriptional
homeodomain repressor CCAAT displacement protein.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF239243; AAF63491.1; -.
DR InterPro; IPR000286; -.
DR Pfam; PF00850; Hist_deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
SQ SEQUENCE 855 AA; 92363 MW; 3157426AE1913DB6 CRC64;

Query Match 47.8%; Score 43; DB 4; Length 855;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPGYGNPHYYA 11
|||||
DB 729 DPPMGDPPEYLA 739

RESULT 13

Q9UFU7 ID Q9UFU7 PRELIMINARY; PRT; 878 AA.
AC Q9UFU7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 94.3 KDA PROTEIN (FRAGMENT).
GN DKFZP586J0917.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Koehler K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117455; CAB55935.1; -.
DR InterPro; IPR000286; -.
DR InterPro; IPR001781; -.
DR Pfam; PF00850; Hist_deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
DR Probom; PD000094; -; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 878 AA; 94329 MW; 26882E693960E10D CRC64;

Best Local Similarity 61.5%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PPGYGNPHYYAMY 14
|||||
DB 77 PPGYGNPHYYAMY 89

RESULT 10

Q9H7L0 ID Q9H7L0 PRELIMINARY; PRT; 484 AA.
AC Q9H7L0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FLJ00062 PROTEIN (FRAGMENT).
GN FLJ00062.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Ohara O., Nagase T., Kikuno R., Okumura K.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
spleen.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024469; BAB15759.1; -.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 484 AA; 52327 MW; 1B1B0B363436A800 CRC64;

Query Match 47.8%; Score 43; DB 4; Length 484;
Best Local Similarity 63.8%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPGYGNPHYYA 11
|||||
DB 298 DPPMGDPPEYLA 308

RESULT 11

Q9NW41 ID Q9NW41 PRELIMINARY; PRT; 614 AA.
AC Q9NW41;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CNA FLJ10328 FIS, CLONE NT2RM2000588, WEAKLY SIMILAR TO HISTONE
DEACETYLASE HDAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RP "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001190; BAA91545.1; -.
DR InterPro; IPR000286; -.
DR Pfam; PF00850; Hist_deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
SQ SEQUENCE 614 AA; 66173 MW; 36C82D314014F211 CRC64;

Query Match 47.8%; Score 43; DB 4; Length 878;
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPPYGNPHYA 11
 ||| | | | |
 DB 692 DPPMGDPYLA 702

RESULT 14
 Q9JL72 PRELIMINARY; PRT; 938 AA.

AC Q9JL72;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HISTONE DEACETYLASE 7.
 GN HDAC7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6:C57BL/6;
 RX MEDLINE=20107033; PubMed=10640276;
 RA Kao H.Y., Downes M., Ordentlich P., Evans R.M.;
 RT "Isolation of a novel histone deacetylase reveals that class I and
 class II deacetylases promote SMRT-mediated repression.";
 RL Genes Dev. 14:55-66(2000).
 DR ENBL; AF207749; AAF31419.1; -.
 DR InterPro; IPR000286; -.
 DR Pfam; PF00850; Hist_deacetyl; 1.
 DR PRINTS; PRO1270; HDASUPER.
 SQ SEQUENCE 938 AA; 101318 MW; A282A36EBC840897 CRC64;

Query Match 47.8%; Score 43; DB 11; Length 938;
 Best Local Similarity 63.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPPYGNPHYA 11
 ||| | | | |
 DB 753 DPPMGDPYLA 763

RESULT 15
 O84688 PRELIMINARY; PRT; 1080 AA.

AC O84688;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PP2-TRANSGLYCOLASE/TRANSEPTIDASE.
 GN PPPB.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UW-3/CX;
 RX MEDLINE=9900809; PubMed=9784136;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 Chlamydia trachomatis";
 RL Science 282:754-759(1998).
 DR EMBL; AE001338; AAC68277.1; -.
 DR InterPro; IPR001460; -.
 DR Pfam; PF00905; Transpeptidase; 1.
 SQ SEQUENCE 1080 AA; 123959 MW; EE647FA87F1FFEDD CRC64;

Query Match 47.8%; Score 43; DB 2; Length 1080;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPPYGNPHY 9
 ||| | | | |
 DB 662 EPPLGNPHY 670

Search completed: June 28, 2001, 16:08:26
 Job time: 954 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:37 ; Search time 362.28 Seconds
(without alignments)
18.575 Million cell updates/sec

Title: US-09-724-406-26

Perfect score: 578

Sequence: 1 DIVLTQSPASLAVSLGRAT.....CQHSGLPFTFGSKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
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12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
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19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526	91.0	212	15	AA052659
2	524	90.7	111	21	AA010019
3	521	90.1	131	13	AA028668
4	520	90.0	111	17	AA085236
5	513.5	88.8	110	15	AA060564
6	513.5	88.8	110	20	AA039532
7	512	88.6	112	16	AA080272
8	510	88.2	111	22	AA069661
9	509	88.1	125	12	AA015440
10	508	87.9	111	15	AA060528
11	505	87.4	112	16	AA075431

12	502.5	86.9	151	22	AA035100	Antibody variable
13	502	86.9	132	17	AA003723	Anti-human gp39 MA
14	500	86.5	218	16	AA075457	Mouse antibody PB3
15	500	86.5	218	16	AA075459	Mouse antibody F4-
16	494	85.5	437	19	AA037738	Nucleotide sequenc
17	489.5	84.7	146	18	AA019578	Mouse anti-idiotyp
18	486.5	84.2	124	12	AA015442	Light chain variab
19	485	83.9	111	10	AA090541	Immunoglobulin L c
20	485	83.9	131	10	AA090543	Amino acids sequen
21	484.5	83.8	110	21	AA090821	317G5 hybridoma VL
22	484.5	83.8	112	11	AA007456	N-terminal sequenc
23	482.5	83.5	110	18	AA022952	Monoclonal antibod
24	482.5	83.5	110	20	AA086119	Murine 340 VL amin
25	480	83.3	111	15	AA055123	Mouse anti-HIV mu5
26	480	83.3	111	15	AA060302	Anti HIV antibody
27	480	83.3	238	19	AA083042	Anti-Fas MAB HF7A
28	480	83.3	238	21	AA014748	Mouse anti-Fas ant
29	480	83.3	238	21	AA090898	Murine anti-Fas an
30	479	82.9	111	21	AA059267	Antibody 4H5 L cha
31	479	82.9	111	21	AA051144	Murine derived pro
32	479	82.9	111	21	AA051146	Murine derived pro
33	479	82.9	132	16	AA070189	Mouse MAB 3B9 ligh
34	479	82.9	132	20	AA023767	Light chain variab
35	479	82.9	132	20	AA018120	Light chain sequen
36	479	82.9	305	21	AA059264	Antibody 4H5 H cha
37	479	82.9	305	21	AA059265	Antibody 4H5 L cha
38	479	82.9	305	21	AA051141	Murine derived pro
39	479	82.9	305	21	AA051142	Murine derived pro
40	476.5	82.4	110	16	AA074957	Immunoglobulin lig
41	476.5	82.4	130	16	AA074957	Anti-idiotyp anti
42	473.5	81.9	110	16	AA074956	Immunoglobulin lig
43	473.5	81.9	146	16	AA074966	Anti-idiotyp anti
44	473	81.8	113	22	AA071895	Monoclonal antibod
45	472	81.7	131	18	AA034516	Variable kappa cha

ALIGNMENTS

RESULT 1
AA052659
ID AA052659 standard; Protein; 212 AA.
XX
AC AA052659;
XX
DT 16-JAN-1995 (first entry)
XX
DE Porphyryn antibody light chain.
XX
KW Light; heavy; chain; monoclonal antibody; porphyrin;
XX absorption spectrum; oxidase activity.
OS Mus musculus.
PN JP06105686-A.
XX
PD 19-APR-1994.
XX
PF 28-SEP-1992; 92JP-0258584.
XX
PR 28-SEP-1992; 92JP-0258584.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 1994-163128/20.
XX N-PSDB; AA062631.
PT Gene encoding monoclonal antibody against porphyrin - useful to
PT produce antibody with modified properties, to interact with e.g.
PT P450, haemoglobin; etc.
XX
PS Claim 4; Page 10-11; 16pp; Japanese.
XX

CC The sequences given in AAR52659-60 represent the light and heavy chains
 CC respectively of a monoclonal antibody which specifically recognises
 CC a specified porphyrin molecule. Using the genes encoding these
 CC proteins, the porphyrin antibody can be mass produced inexpensively.
 CC Features of the porphyrin monoclonal antibody may be modified, eg.
 CC absorption spectrum shift and expression of oxidase activity, by
 CC alterations within the coding region.

XX
 SQ Sequence 212 AA;

Query Match 91.0%; Score 526; DB 15; Length 212;
 Best Local Similarity 91.0%; Pred. No. 1.le-37;
 Matches 101; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 Db 1 divltqspaslavslgqratiscrasksvasgylymhwqqgppkllislatnles 60
 QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
 Db 61 gvparfsgsggdtftlnhpveeedvatycqhsrelptftgagtklelk 111

RESULT 2

AAB10019
 ID AAB10019 standard; Protein; 111 AA.

XX
 AC AAB10019;

XX
 DT 01-NOV-2000 (first entry)

XX
 DE H. pylori HSP60-binding antibody light chain protein.

XX
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heat shock protein; HSP60; light chain.

XX
 OS Unidentified.

XX
 PN WO200026671-A1.

XX
 PD 11-MAY-2000.

XX
 PF 29-OCT-1999; 99WO-EP09212.

XX
 PR 29-OCT-1998; 98EP-0120517.

XX
 PR 06-NOV-1998; 98EP-0120687.

XX
 PA (CONN-) CONNEX GMBH.

XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringels A;

XX
 DR WPI; 2000-365747/31.

XX
 DR N-PSDB; AAA40199.

XX
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage

XX
 PS Disclosure; Fig 1; 84pp; German.

XX
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (MAb) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display

CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents the H. pylori heat shock protein, HSP60-binding
 CC antibody (DMS ACC2356) light chain which is used to illustrate the method
 CC of the invention.

XX
 SQ Sequence 111 AA;

Query Match 90.7%; Score 524; DB 21; Length 111;
 Best Local Similarity 90.1%; Pred. No. 8.4e-38;
 Matches 100; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 Db 1 divltqspaslavslgqratiscrasksvstsgysyihwyqqgppklliflasnles 60

QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111

Db 61 gvparfsgsggdtftlnhpveeedaatyhcqhsrelptftgagtklelk 111

RESULT 3

AAR28668
 ID AAR28668 standard; Protein; 131 AA.

XX
 AC AAR28668;

XX
 DT 30-MAR-1993 (first entry)

XX
 DE p12-k2.

XX
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
 KW plasmid; p12-k2; p12-h2.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FH Peptide 1..20

FT FT /note= "Signal peptide"

FT FT 21..131
 FT FT /note= "Mature peptide"

XX
 PN WO9219759-A.

XX
 PD 12-NOV-1992.

XX
 PF 24-APR-1992; 92WO-JP00544.

XX
 PR 25-APR-1991; 91JP-0095476.

XX
 PR 19-FEB-1992; 92JP-0032084.

XX
 PA (CHUS) CHUGAI SEIYAKU KK.

XX
 PI Bendig MM, Jones ST, Saidanha JW, Sato K, Tsuchiya M;

XX
 DR WPI; 1992-398882/48.

XX
 DR N-PSDB; AAQ30753.

XX
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions

XX
 PS Disclosure; Page 118; 207pp; Japanese.

XX
 CC The sequences given in AAR28668-69 were encoded by plasmid sequences
 CC which were used in example to illustrate the production of a human

CC antibody which recognises human interleukin-6 receptor (IL-6R). The
CC antibody comprises light (L) chain and heavy (H) chain variable
CC regions which were derived from a mouse monoclonal antibody produced
CC from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
CC p12-h2.
XX
SQ Sequence 131 AA;

Query Match 90.1%; Score 521; DB 13; Length 131;
Best Local Similarity 90.1%; Pred. No. 1.8e-37;
Matches 100; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
Db 21 divltqspaslgvslgratiscrasksvstsgysymhwyyqgkpgqpkllilylasnles 80

Qy 61 GVPARFSGSGGTDFTLNIHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
Db 81 gvparfsgsgsgtdftlnihpveedaatyycqhsrenpytfgggtkleik 131

RESULT 4
AAR85236
ID AAR85236 standard; Protein; 111 AA.
XX
AC AAR85236;
XX
DT 05-APR-1996 (first entry)
XX
DE Murine 206 antibody variable light chain region.
XX
KW Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
KW infection; detection; isolation; monoclonal antibody; MAB; mimetic;
KW humanised; murine; heavy chain; light chain; variable region; CDR;
KW NEWM; REI.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Binding-site 24..38
FT /label= CDR 1.
FT Binding-site 54..60
FT /label= CDR 2.
FT Binding-site 93..101
FT /label= CDR 3.
XX
PN WO9531546-A1.
XX
PD 23-NOV-1995.
XX
PF 28-APR-1995; 95WO-US05305.
XX
PR 28-APR-1994; 94US-0234133.
XX
PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
XX
PI Carr FJ, Harris WJ, Moss MT, Wallace TP;
XX
DR WPI; 1996-010932/01.
DR N-PSDB; AAT06051.
XX
PT Varicella zoster virus gpIII antibody with humanised variable region
PT - for treatment, prevention or diagnosis of varicella zoster virus
PT infections
XX
PS Claim 2; Figure 2; 58pp; English.
XX
CC Antibodies (Ab) comprising a humanised variable region specifically
CC binding to a varicella zoster virus (VZV) can be used to treat or
CC prevent VZV infection. They may optionally be attached to a
CC therapeutic agent. They may also be used, when labelled, to detect
CC VZV particles and infected cells in blood; for the removal/
XX

CC neutralisation of infectious VZV in blood; for the selection/
CC isolation of human monoclonal Abs and for the design of (non-)
CC peptide mimetics with similar diagnostic and therapeutic uses. The
CC variable region CDR portion is derived from murine Ab 206 and the
CC heavy and light chain variable region frameworks are NEWM and REI
CC respectively. The framework may include at least one mutation that
CC improves binding specificity or affinity. The heavy and light chain
CC variable regions are preferably (VZVHu-VH, -VHKFIIIS, -VHTLY,
CC -VHKVRSE or -VHS) and VZVHuVH respectively.
XX
SQ Sequence 111 AA;

Query Match 90.0%; Score 520; DB 17; Length 111;
Best Local Similarity 91.0%; Pred. No. 1.8e-37;
Matches 101; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
Db 1 divltqspas..avslgratiscrasksvstsgssymhwyyqgkpgqpkllilylasnles 60

Qy 61 GVPARFSGSGGTDFTLNIHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
Db 61 gvlsrfsgsgsgtdftlnihpveedaatyycqhsrelpftfgpgtkleik 111

RESULT 5
AAR60564
ID AAR60564 standard; Protein; 110 AA.
XX
AC AAR60564;
XX
DT 25-APR-1995 (first entry)
XX
DE Anti-carcinoembryonic antigen chimeric light chain Ab.
XX
KW Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW chimeric human-murine; breast or colorectal carcinoma;
KW light chain.
XX
OS Chimeric Mus muscaris.
OS Chimeric Homo sapiens.
XX
PN WO9419466-A.
XX
PD 01-SEP-1994.
XX
PF 16-FEB-1994; 94WO-US01709.
XX
PR 16-FEB-1993; 93US-0017570.
XX
PA (DOWC) DOW CHEM CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Gourlie BB, Kaplan DA, Mezes PS, Rixon MW, Schlom J;
XX
DR WPI; 1994-294331/36.
DR N-PSDB; AAQ71394.
XX
PT Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis
PT and therapy of carcinoma, e.g. breast or colorectal carcinoma
XX
PS Claim 11; Page 50; 67pp; English.
XX
CC AAQ71394 codes for AAR60564 the antibody light chain region of
CC murine-human anti-carcinoembryonic antigen (CEA) chimeric
CC antibody. Which can be used in in vitro immunoassays for
CC the detection of CEA, and monitoring of tumour-associated
CC antigen during therapy. It can also be used in vivo diagnostically,
CC or in therapy for the treatment of tumours associated with
CC colorectal and breast carcinomas, as well those of the
CC gastrointestinal tract, lung, ovary and pancreas.
XX

SQ Sequence 110 AA;

Query Match 88.8%; Score 513.5; DB 15; Length 110;
Best Local Similarity 90.1%; Pred. No. 6.5e-37;
Matches 100; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
DB 1 divltspasltvslglratiscrasksvasgysymhwyrpqpqppkllilylasnlqs 60
QY 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGELPFTFGSGTKLEIK 111
DB 61 gvparfsgsgsgtdftlnhpveeedaatyqchsrelp-tfgggtkleik 110

RESULT 6

AAV39532
ID AAY39532 standard; protein; 110 AA.

XX AAY39532;

DT 22-NOV-1999 (first entry)

DE Murine COL1 VK chain (COL1MuVK).

KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.

XX Mus sp.

XX WO9943817-A1.

XX 02-SEP-1999.

XX 25-FEB-1998; 98WO-US03680.

XX 25-FEB-1998; 98WO-US03680.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;

XX WPI; 1999-550870/46.

XX New antibody specific for treatment and diagnosis of cancer

PS Claim 2; Fig 2; 82pp; English.

XX This sequence represents the murine COL1 VK chain (COL1MuVK), and was
CC used to obtain the humanised antibody (Ab) of the invention. The
CC humanised Ab, or its fragment, specifically binds to carcinoembryonic
CC antigen (CEA). The Ab, optionally coupled to an effector or label, is
CC used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary,
CC lung, stomach, or colon) and to detect CEA-expressing cells, either in
CC vitro (optionally on a solid support) or in vivo (particularly by tumour
CC imaging to identify tumours and metastases before surgery), for diagnosis
CC or prognosis. It is not significantly immunogenic, i.e. the Ab does not
CC induce a human anti-murine antibody or allergic response, or non-specific
CC cytotoxicity, so can be administered repeatedly. It retains specificity
CC for CEA, and has improved clearance (allowing efficient targeting) and
CC metabolic properties.

XX Sequence 110 AA;

Query Match 88.8%; Score 513.5; DB 20; Length 110;
Best Local Similarity 90.1%; Pred. No. 6.5e-37;
Matches 100; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
DB 1 divltspasltvslglratiscrasksvasgysymhwyrpqpqppkllilylasnlqs 60

QY 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGELPFTFGSGTKLEIK 111
DB 61 gvparfsgsgsgtdftlnhpveeedaatyqchsrelp-tfgggtkleik 110

RESULT 7

AAV80272
ID AAR80272 standard; Protein; 112 AA.

XX AAR80272;

DT 27-FEB-1996 (first entry)

DE V1 region from an antibody against cancer-specific mucin.

KW Antibody; heavy chain; light chain; variable region; cancer; mucin;
KW hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;
KW Fv; human; constant domain; chimera; anaphylaxis.

XX Synthetic.

PH Key Location/Qualifiers

FT Domain 24..38

FT /label= CDR1

FT Domain 54..60

FT /label= CDR2

FT Misc-difference 64

FT /note= "encoded by GAG"

FT Domain 93..101

FT /label= CDR3

XX FR2714915-A1.

XX 13-JUL-1995.

XX 13-JAN-1995; 95FR-0000349.

XX 13-JAN-1994; 94JP-0002131.

XX (TOYJ) TOSOH CORP.

XX Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;

XX WPI; 1995-247908/33.

XX N-PSDB; RAQ98534.

XX New variable domains of antibody recognising cancer specific mucin
PT - and related DNA and expression vectors, producing chimeric
PT mouse-human antibody for diagnosis and treatment of cancer

PS Claim 6; Page 16-17; 25pp; French.

XX The amino acid sequence of the variable region from the light chain of
CC an antibody against cancer-specific mucin. The coding sequence was
CC isolated from N2D hybridoma cells expressing a murine antibody reactive
CC with pancreatic cancer cells. The DNA encoding the antibody variable
CC regions from the heavy (AAQ98533) and light chains were isolated and
CC inserted into vectors. These vectors express the domains as an Fv
CC antibody. Vectors which additionally contain genes encoding the human
CC constant domains express a chimeric mouse-human antibody. The antibodies
CC are useful in the detection and treatment of cancer. The chimeras should
CC be less likely to cause anaphylaxis than the original murine antibody.

XX Sequence 112 AA;

Query Match 88.6%; Score 512; DB 16; Length 112;
Best Local Similarity 87.4%; Pred. No. 8.9e-37;
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
DB 1 divltspasltvslglratiscrasksvasgysymhwyrpqpqppkllilylasnlqs 60

Db 1 divltqspaslavslqgratiscrasksvtsdfsymhwyqkpgppklllylasnles 60
QY 61 GVPARFSGSGGDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
DB 61 gvpdrfsgsgsgtdftlnihpveedaatyqchsrefpwtfggggkkleik 111

RESULT 8
AAB69661
ID AAB69661 standard; Protein; 111 AA.
XX
AC AAB69661;
DT 30-APR-2001 (first entry)
XX
DE Murine Fd79 antibody light chain SEQ ID NO: 46.
XX
KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
OS Mus sp.
XX
PN US6180370-B1.
XX
PD 30-JAN-2001.
XX
PF 07-JUN-1995; 95US-0484537.
XX
PR 28-DEC-1988; 88US-0290975.
PR 13-FEB-1989; 89US-0310252.
PR 28-SEP-1990; 90US-0590274.
PR 19-DEC-1990; 90US-0634278.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Queen CL, Sellick HE;
XX
DR WPI; 2001-190856/19.
XX
PT Producing humanized immunoglobulin, involves producing a cell
PT containing DNA segments encoding humanized heavy and light chain
PT variable regions, and expressing the DNA segments in the cell -
XX
PS Example 6; Fig 2; 145pp; English.
XX
CC The present invention describes a method of producing humanised
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a
CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of
CC graft-versus-host disease, transplant rejection, autoimmune diseases such
CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
CC and systemic lupus erythematosus, herpes infections, CMV virus infections
CC and myeloid leukaemia. The present sequence is an antibody used to
CC demonstrate the method of the invention.
XX
SQ Sequence 111 AA;

Query Match 88.2%; Score 510; DB 22; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.3e-36;
Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNYMHVYQQAGOPPCKLLIHLASNLES 60
DB 1 divltqspaslavslqgratiscrasksvststynmhwyqkpgppkllikyasnles 60

QY 61 GVPARFSGSGGDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
DB 61 gvpdrfsgsgsgtdftlnihpveedaatyqchsrefpwtfggggkkleik 111

RESULT 9
AAR15440
ID AAR15440 standard; Protein; 125 AA.
XX
AC AAR15440;
DT 25-FEB-1992 (first entry)
XX
DE Light chain variable region of MAb 2C2.
XX
KW HRV; ICAM-1; antigen-binding fragment; inflammation;
KW auto-immune disease.
XX
OS Homo sapiens.
XX
PN EP459577-A.
XX
PD 04-DEC-1991.
XX
PF 25-MAY-1991; 91EP-0201243.
XX
PR 01-JUN-1990; 90US-0532001.
XX
PA (MERI) MERCK & CO INC.
XX
PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
XX
DR WPI; 1991-355850/49.
XX
PT Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
XX
PS Claim 1; Page 20; 28pp; English.
XX
CC This is one of six antibody fragments from MAb's specific for domain
CC 1 of ICAM-1. The peptide fragments can be used to treat or prevent
CC rhinovirus infection. See AAR15437-R15443.
XX
SQ Sequence 125 AA;

Query Match 88.1%; Score 509; DB 12; Length 125;
Best Local Similarity 87.4%; Pred. No. 1.8e-36;
Matches 97; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNYMHVYQQAGOPPCKLLIHLASNLES 60
DB 1 divltqspaslavslqgratiscrasksvststfsmhwyqkpgppkllikfasnles 60

QY 61 GVPARFSGSGGDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
DB 61 gvpdrfsgsgsgtdftlnihpveedaatyqchsrefpwtfggggkkleik 111

RESULT 10
AAR60528
ID AAR60528 standard; Protein; 111 AA.
XX
AC AAR60528;
DT 07-APR-1995 (first entry)
XX
DE Light chain variable region of monoclonal antibody 5E8.
XX
KW Secretion sequence; vector; antibody; single chain antibody;
KW promoter; Bacillus subtilis; ss.
XX
OS Synthetic.
XX
PN EP614982-A.
XX

PD 14-SEP-1994.
 XX
 PF 05-MAR-1994; 94EP-0200564.
 XX
 PR 10-MAR-1993; 93IT-OMI0456.
 XX
 PA (ENIE) ENIRICERHE SPA.
 XX
 XX Cuzzoni A, De FERRA F, Grandi G, Tortora O, Tosi C;
 XX WPI; 1994-281209/35.
 XX DR N-PSDB; AAQ71286.
 XX
 PT Vector for secretion of single chain antibody from Bacillus
 PT subtilis - contg. neutral protease promoter and specific leader
 PT sequence, providing high yield of soluble antibody for diagnostic
 PT or therapeutic use
 XX
 XX Example 3; Figure 2; 27pp; English.
 PS
 CC The sequence encoding the variable region of the light chain of the
 CC monoclonal antibody 5p8 (specific for the alpha subunit of human
 CC gonadotrophin) was amplified for its use in a recombinant vector
 CC which also comprised (1) the promoter of the gene for the neutral
 CC protease of Bacillus subtilis BGSC IA341, (2) the secretion sequence
 CC described in AAQ71278. The amplified fragment was used to produce a
 CC DNA sequence encoding an antibody in single molecule form with the
 CC sequence VH/VK-L-VK/(TAG)n, where VH and VK are the variable
 CC regions of the heavy and light chains of the antibody and L is the
 CC linker of sequence Val-Ser-Ser-(Gly(4)-Ser)3. TAG is a peptide
 CC recognised by polyclonal antibodies directed towards the same peptide,
 CC n is 1 or 0. The vector is used for the production of single chain
 CC antibodies which have improved pharmacokinetic properties and can be
 CC produced more economically than monoclonal antibodies. The vector
 CC allows production of antibodies in completely soluble form with
 CC secretion in high yield.
 XX
 SQ Sequence 111 AA;
 Query Match 87.9%; Score 508; DB 15; Length 111;
 Best Local Similarity 89.1%; Pred. No. 1.9e-36;
 Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 DB 1 diggtqspaslvslgqratiscrasksvasgysvnyvqkpgppklliyasnl 60
 QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEI 110
 DB 61 gvparfsgsgsgtdftlnhpveeedaatycqhsrelptlftfgagtklei 110
 RESULT 11
 AAR75431
 ID AAR75431 standard; Protein; 112 AA.
 XX
 AC AAR75431;
 XX
 DT 01-FEB-1996 (first entry)
 XX
 DE Human thyroid stimulating hormon antibody light chain variable.
 XX
 KW thyroid stimulating hormone; TSH; human; variable region; heavy;
 KW chain; antibody; chimeric antibody.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 24..38
 FT /note= "Complementarity determining region (CDR) 1"
 FT 54..60
 FT /note= "CDR2"

FT Region 93..101
 FT /note= "CDR3"
 XX
 PN JP07132097-A.
 XX
 PD 23-MAY-1995.
 XX
 PF 28-JUN-1993; 93JP-0156707.
 XX
 PR 28-JUN-1993; 93JP-0156707.
 XX
 XX (TOYJ) TOSOH CORP.
 XX
 XX WPI; 1995-220118/29.
 XX DR N-PSDB; AAQ74148.
 XX
 PT DNA encoding an antibody recognising human thyroid-stimulating
 PT hormone - and preparation of chimeric antibody by expressing the
 PT DNA in a transformed host cell
 XX
 PS Claim 8; Fig 4; 8pp; Japanese.
 XX
 CC The sequence is the light chain variable region of an antibody
 CC recognising human thyroid stimulating hormone (hTSH). Prepn. of a
 CC chimeric antibody by expressing the DNA in a transformed host cell
 CC is also claimed. The anti-hTSH antibody has an additional useful
 CC function which could not be given by a mouse derived anti-TSH monoclonal
 CC antibody (sic).
 XX
 SQ Sequence 112 AA;
 Query Match 87.4%; Score 505; DB 16; Length 112;
 Best Local Similarity 86.5%; Pred. No. 3.5e-36;
 Matches 96; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 DB 1 divltqspaslvslgqratiscrasksvasgysvnyvqkpgppkllikfasnl 60
 QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEI 111
 DB 61 gvparfsgsgsgtdftlnhpveeedaatycqhtweiprtfgggtkleik 111
 RESULT 12
 AAB35100
 ID AAB35100 standard; Protein; 151 AA.
 XX
 AC AAB35100;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Antibody variable region fusion protein #4.
 XX
 KW Filamentous phage; protein display; pVII; pIX;
 KW combinatorial antibody library.
 XX
 OS Synthetic.
 XX
 PN WO200071694-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000WO-US14433.
 XX
 PR 25-MAY-1999; 99US-0318786.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Janda KD, Wirsching P, Lerner RA, Gao C;
 XX WPI; 2001-032030/04.

XX Novel filamentous phage encapsulating a genome encoding fusion
PT polypeptide comprising exogenous polypeptide fused to amino terminus of
PT pVII and pIX proteins, for constructing diverse heterodimeric
PT polypeptide array -
XX
XX Example 1: Page 82-83; 90pp; English.
XX
CC The present invention describes a filamentous phage encapsulating a
CC genome encoding a fusion protein. This fusion protein comprises an
CC exogenous protein fused to the amino terminus of a filamentous phage pVII
CC or pIX protein. This is useful in the design of proteins for medical,
CC industrial, environmental and research applications.
XX
XX Sequence 151 AA;
XX
Query Match 86.9%; Score 502.5; DB 22; Length 151;
Best Local Similarity 88.4%; Pred. No. 7.8e-36;
Matches 99; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSASGYNMHWYQOKAGOPPKLLIHLASNL 60
DB 1 divltqspaslavslgqratiscrasksvstsgynmhwqqkpgppklliyasnlas 60
QY 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
DB 61 gvparfsgsggtdftlnhnpveedaatyyclysfrefpwtfgggtkileik 112
XX
RESULT 13
AAW03723
ID AAW03723 standard; Protein; 132 AA.
XX
AC AAW03723;
XX
XX 02-APR-1997 (first entry)
XX
XX Anti-human gp39 MAb 39-1.7 light chain variable region.
XX
XX Light chain; variable region; murine; mouse; anti-human; disease;
KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.7; hybridoma;
KW diagnosis; inhibition; B-cell; activation; treatment; disorder;
KW immune; autoimmune; allergic response; organ rejection; drug;
KW graft versus host; cell imaging; tumour; targeted; delivery;
KW targeted.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= sig_peptide
XX Peptide 21..132
XX /label= mat_peptide
XX Region 44..58
XX /note= "complementarity determining region 1"
XX Region 74..80
XX /note= "complementarity determining region 2"
XX Region 113..121
XX /note= "complementarity determining region 3"
XX
XX WO9623071-A2.
XX
XX 01-AUG-1996.
XX
XX 26-JAN-1996; 96WO-US01119.
XX
XX 26-JAN-1995; 95US-0379057.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;
PI Harris LJ, Hollenbaugh D, Sladak AW;

XX WPI: 1996-362694/36.
DR N-PSDB; AAT35975.
XX
PT Monoclonal antibodies specific for different epitope(s) on human
PT gp39 - used for inhibiting B cell activation and for the diagnosis
PT of various disorders, e.g. cancer, psoriasis etc..
XX
XX Claim 93; Fig 7A; 167pp; English.
XX
CC The present sequence is the light chain variable region of the
CC murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAB)
CC 39-1.7 (a member of the murine kappa II subfamily). The MAB was
CC prep'd. by immunising a 6-8 week old BALB/c mouse with a gp39-CD8
CC fusion protein, and 3 days later harvesting and fusing spleen and
CC lymph cells to mouse melanoma cells, to produce an anti-human gp39
CC MAB producing hybridoma. The MAB may be useful for diagnosing
CC disease states, inhibiting B-cell activation and for treating
CC immunological disorders, e.g. autoimmune disorders, allergic
CC responses, organ rejection and graft versus host disease. It may
CC also be used for imaging cells which express gp39 on their surface,
CC e.g. tumour cells, and to target therapeutic agents to such cells.
CC The MAB inhibits the CD40/gp39 interaction, therefore limiting both
CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.
CC specific to these antigens. A typical compsn. for intramuscular
CC injection pref. contains 50 mg of MAB in 1 ml of sterile buffered
CC water.
XX
XX Sequence 132 AA;
XX
Query Match 86.9%; Score 502; DB 17; Length 132;
Best Local Similarity 86.5%; Pred. No. 7.5e-36;
Matches 96; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSASGYNMHWYQOKAGOPPKLLIHLASNL 60
DB 21 divltqspaslavslgqratiscrasksvstsgynmhwqqkpgppklliyasnl 80
QY 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
DB 81 gvparfsgsggtdftlnhnpveedaatyycqhsweipftfgsgtkleir 131
XX
XX RESULT 14
XX AAR75457
XX ID AAR75457 standard; Protein; 218 AA.
XX
XX AC AAR75457;
XX
XX 07-FEB-1996 (first entry)
XX
XX Mouse antibody F33-2 light chain variable region protein sequence.
XX
XX Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KW antibody; immunotolerance; animal; variegated display library;
KW variable region; antigen; immunorecessive; cell surface marker; foetal;
KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KW familial hypercholesterolaemia; binding affinity.
XX
XX Mus musculus.
XX
XX WO9515982-A2.
XX
XX 15-JUN-1995.
XX
XX 08-DEC-1994; 94WO-US14106.
XX
XX 06-DEC-1994; 94US-0350400.
XX 08-DEC-1993; 93US-0164022.
XX
XX (GENZ) GENZYME CORP.
XX

PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
XX
DR WPI; 1995-224291/29.
DR N-PSDB: AAO92501.

PT Generating new antibodies specific for immunorecessive epitopes -
PT by selection from variegated V gene library cloned from
PT immuno:tolerance derived antibody repertoire, useful in diagnosis,
PT purifcn. and therapy, e.g. of cancer
XX
PS Disclosure: Page 76-77: 109pp: English:

The sequence of the light chain variable region from the mouse antibody F3-2. This sequence was isolated from a repertoire display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AAQ74153-74. The variable regions, esp the complementarity determining regions (CDR; see AAR/5462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a tumorecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by combinatorial/hybridoma methods.

Sequence 218 AA;

Query Match	86.5%	Score 500;	DB 16;	Length 218;
Best Local Similarity	84.7%	Pred. No. 1.9e-35;		
Matches 94;	Conservative	7;	Mismatches 10;	Indels 0;
Gaps	0;			

(GENZ) GENZYME CORP.
Barsomian G, Copeland DP, Hillhouse D, Johnson T;
WPI; 1995-224291/29.
N-PSDB; AAQ92503.

The sequence of the light chain variable region from the mouse antibody F4-7. This sequence was isolated from a variegated display library (VDL) of variable regions derived from a repertoire of antibodies from an immunotolerised animal. The VDL is generated by PCR amplifying the variable regions from the antibody coding sequences using the primers AA074153-74. The variable regions, esp the complementarity determining regions (CDR; see AAR75462-93 for examples of CDRs) from the immunotolerant animals' antibodies are used to construct an antibody against a immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or stem cell, which can differentiate between variant or related forms of the antigen. The antibodies generated can be used in the diagnosis, e.g. detection of the immunorecessive antigen, or in therapy e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia. The method of production of the antibody allows rapid and sensitive isolation of antibodies that would be difficult to isolate by standard methods. The antibodies produced have greater binding affinity than those produced by combinatorial/hybridoma methods.

Sequence 218 AA;

Query Match 86.5%; Score 500; DB 16; Length 218;
Best Local Similarity 84.7%; Pred. No. 1.9e-35;
Matches 94; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Search completed: June 28, 2001, 16:14:38
Job time: 1326 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:15 ; Search time 138.34 Seconds
(without alignments)
16.163 Million cell updates/sec

Title: US-09-724-406-26
Perfect score: 578
Sequence: 1 DIVLTQSPASVSLQRAT.....COHSGELPTFGSGTKLEIK 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	90.1	131	1	US-08-137-117D-25
2	521	90.1	131	2	US-08-436-717-25
3	513.5	88.8	110	1	US-08-017-570-2
4	513.5	88.8	110	1	US-08-471-426-2
5	513.5	88.8	110	5	PCT-US94-01709-2
6	510	88.2	111	1	US-07-634-278-46
7	510	88.2	111	1	US-08-477-728-46
8	510	88.2	111	1	US-08-474-040-46
9	510	88.2	111	1	US-08-487-200-46
10	510	88.2	111	4	US-08-484-537-46
11	508	87.9	111	1	US-08-207-169A-4
12	505	87.4	111	5	PCT-US94-14106-53
13	502	86.9	132	2	US-08-379-057-16
14	500	86.5	218	5	PCT-US94-14106-57
15	489.5	84.7	146	2	US-08-653-402B-12
16	484.5	83.8	110	3	US-08-483-749A-20
17	479	82.9	132	2	US-08-483-636-2
18	479	82.9	132	2	US-08-483-632-2
19	475	82.2	111	1	US-08-491-845-8
20	474	82.0	131	4	US-08-579-378A-14
21	472	81.7	131	3	US-08-589-939-3
22	461	79.8	106	3	US-08-466-151-6
23	460.5	79.7	110	1	US-08-442-542-8
24	460.5	79.7	110	3	US-08-765-469-8
25	453	78.4	120	1	US-08-111-080-26
26	453	78.4	120	1	US-08-211-980-26
27	453	78.4	120	5	PCT-US93-07967-26

28	452.5	78.3	112	2	US-08-888-366-18	Sequence 18, Appl
29	450	77.9	111	1	US-08-275-053-11	Sequence 11, Appl
30	450	77.9	111	3	US-08-466-151-2	Sequence 2, Appl
31	450	77.9	121	1	US-08-111-080-22	Sequence 22, Appl
32	450	77.9	121	1	US-08-211-980-22	Sequence 22, Appl
33	450	77.9	121	5	PCT-US93-07967-22	Sequence 22, Appl
34	447	77.3	120	1	US-08-111-080-24	Sequence 24, Appl
35	447	77.3	120	1	US-08-211-980-24	Sequence 24, Appl
36	447	77.3	120	5	PCT-US93-07967-24	Sequence 24, Appl
37	446	77.2	111	1	US-07-634-278-54	Sequence 54, Appl
38	446	77.2	111	1	US-08-477-728-54	Sequence 54, Appl
39	446	77.2	111	1	US-08-474-040-54	Sequence 54, Appl
40	446	77.2	111	1	US-08-487-200-54	Sequence 54, Appl
41	446	77.2	111	4	US-08-484-537-54	Sequence 54, Appl
42	446	77.2	131	1	US-07-634-278-67	Sequence 67, Appl
43	446	77.2	131	1	US-08-477-728-67	Sequence 67, Appl
44	446	77.2	131	1	US-08-474-040-67	Sequence 67, Appl
45	446	77.2	131	1	US-08-487-200-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-08-137-117D-25
; Sequence 25, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: WO PCT/Jp92/00544
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid

US-08-436-717-25

RESULT 4

US-08-471-426-2
; Sequence 2, Application US/08471426
; Patent No. 5808033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-2

Query Match 88.8%; Score 513.5; DB 1; Length 110;
Best Local Similarity 90.1%; Pred. No. 3.1e-47;
Matches 100; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNHYMHYQKAGOPPKLLIHLASNL 60
Db 1 DIVLTQSPASLTVSLGLRATISCRASKSVASGYNHYMHYQKAGOPPKLLIHLASNL 60
QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
Db 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELP-TFGGSGTKLEIK 110

RESULT 5
PCT-US94-01709-2
; Sequence 2, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI

COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01709-2

Query Match 88.8%; Score 513.5; DB 5; Length 110;
Best Local Similarity 90.1%; Pred. No. 3.1e-47;
Matches 100; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNHYMHYQKAGOPPKLLIHLASNL 60
Db 1 DIVLTQSPASLTVSLGLRATISCRASKSVASGYNHYMHYQKAGOPPKLLIHLASNL 60
QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
Db 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELP-TFGGSGTKLEIK 110

RESULT 6
US-07-634-278-46
; Sequence 46, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-46

Query Match 88.28; Score 510; DB 1; Length 111;
Best Local Similarity 88.38; Pred. No. 7.2e-47;
Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHYQKAGQPPKLLIHLASNL 60
|||||
DB 1 DIVLTQSPASLAVSLGORATISCRASQSVSTSYNMHWYQKQGPQPKLLIKYASNL 60
|||||
QY 61 GVPARFSGSGTGDTLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
|||||
DB 61 GVPARFSGSGTGDTLTNIHPVEEDASTYYCQHSWEIPVTFGGGTKLEIK 111
|||||

RESULT 9
US-08-487-200-46
Sequence 46, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Map Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-46

Query Match 88.28; Score 510; DB 1; Length 111;
Best Local Similarity 88.38; Pred. No. 7.2e-47;
Matches 98; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHYQKAGQPPKLLIHLASNL 60
|||||
DB 1 DIVLTQSPASLAVSLGORATISCRASQSVSTSYNMHWYQKQGPQPKLLIKYASNL 60
|||||
QY 61 GVPARFSGSGTGDTLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
|||||
DB 61 GVPARFSGSGTGDTLTNIHPVEEDASTYYCQHSWEIPVTFGGGTKLEIK 111
|||||

RESULT 10
US-08-484-537-46
Sequence 46, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Map Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-46

Query Match 88.2%; Score 510; DB 4; Length 111;
Best Local Similarity 88.3%; Pred. No. 7.2e-47; Indels 0; Gaps 0;
Matches 98; Conservative 3; Mismatches 10;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMYHWYQKAGQPPKLLIHLASNL 60

DB 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSYNMYHWYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

DB 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 11

US-08-207-169A-4

Sequence 4, Application US/08207169A
Patent No. 5674712

GENERAL INFORMATION:

APPLICANT: GRANDI, GUIDO

APPLICANT: DE PERRA, FRANCESCA

APPLICANT: TOSI, CLAUDIO

APPLICANT: TORTORA, ORNELLA

APPLICANT: CUZZONI, ANNA

TITLE OF INVENTION: RECOMBINANT VECTOR AND USE THEREOF FOR

TITLE OF INVENTION: EXCELLULAR PREPARATION OF SINGLE MOLECULA ANTIBODIES FROM

TITLE OF INVENTION: BACILLUS SUBTILIS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/207,169A

FILING DATE: 08-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5674712man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 2264-061-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-207-169A-4

Query Match 87.9%; Score 508; DB 1; Length 111;
Best Local Similarity 89.1%; Pred. No. 1.2e-46; Indels 0; Gaps 0;
Matches 98; Conservative 6; Mismatches 6;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMYHWYQKAGQPPKLLIHLASNL 60
DB 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMYHWYQKAGQPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 110
DB 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 110

RESULT 12

PCT-US94-14106-53

Sequence 53, Application PC/TUS9414106

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Process for Generating Specific Antibodies

NUMBER OF SEQUENCES: 61

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14106

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-14106-53

Query Match 87.4%; Score 505; DB 5; Length 111;
Best Local Similarity 86.5%; Pred. No. 2.4e-46; Indels 0; Gaps 0;
Matches 96; Conservative 6; Mismatches 9;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMYHWYQKAGQPPKLLIHLASNL 60

DB 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSYNMYHWYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

DB 61 GVPARFSGSGGTDFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 13

US-08-379-057-16

Sequence 16, Application US/08379057

Patent No. 5876950

GENERAL INFORMATION:

APPLICANT: Siadak, Anthony W.

APPLICANT: Hollenbaugh, Diane L.

APPLICANT: Gilliland, Lisa K.

APPLICANT: Gordon, Marcia L.

APPLICANT: Bajorath, Jurgun

APPLICANT: Aruffo, Alejandro A.

TITLE OF INVENTION: Monoclonal Antibodies Specific For

TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use

TITLE OF INVENTION: In Diagnosis and Therapy

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/379,057
: FILING DATE: 26-JAN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Poor, Brian W.
: REGISTRATION NUMBER: 32,928
: REFERENCE/DOCKET NUMBER: ON0133-
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (206) 727-3670
: TELEFAX: (206) 727-3601
:
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 132 amino acids
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: FRAGMENT TYPE: N-terminal
:
: US-08-379-057-16

```

Query Match	86.9%	Score 502;	DB 2;	Length 132;
Best Local Similarity	86.5%	Pred. No. 6.2e-46;		
Matches 96;	Conservative 6;	Mismatches 9;	Indels 0;	Gaps 0;
QY	1	DIVLTQSPASLVSLGQRATISCRASKVSASGYNMHYQQKAGQPKLLIHLASNLFS	60	
Db	21	DIVLTQSPVSLAVSLGQRVTISCRASQSVSSNSTSYMHYQQKPGQPKLLIKYASNLFS	80	
QY	61	GVPAFSGSGGSDFTLNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK	111	
Db	81	GVPAFSGSGGSDFTLNIHPVEEDATYYCQHSWEIPTFGSGTKLEIR	131	

RESULT 14
PCT-US94-14106-57
; Sequence 57, Application PC/TUS9414106
; GENERAL INFORMATION:

```

1 / TITLE OF INVENTION: Process for Generating Specific Antibodies
2 /
3 / NUMBER OF SEQUENCES: 61
4 / COMPUTER READABLE FORM:
5 / MEDIUM TYPE: Floppy disk
6 / COMPUTER: IBM PC compatible
7 / OPERATING SYSTEM: PC-DOS/MS-DOS
8 / SOFTWARE: ASCII (text)
9 /
10 / CURRENT APPLICATION DATA:
11 / APPLICATION NUMBER: PCT/US94/14106
12 / FILING DATE:
13 / CLASSIFICATION:
14 /
15 / INFORMATION FOR SEQ ID NO: 57:
16 / SEQUENCE CHARACTERISTICS:
17 / LENGTH: 218 amino acids
18 / TYPE: amino acid
19 / TOPOLOGY: linear
20 / MOLECULE TYPE: protein
21 / PCT-US94-14106-57

```

Query Match	86.5%	Score 500;	DB 5;	Length 218;
Best Local Similarity	84.7%	Pred. No. 1.8e-45;		
Matches 94;	Conservative 7;	Mismatches 10;	Indels 0;	Gaps 0;

QY	1	DIVLTQSPASLAVSLGQRATISCRASKSVSASGYNMYMHYQQRAGQPPKLLIHLASNL	60
		: : : : : : : : : :	
Db	1	DIVMTQSPASLAVSLGQRATISCRVRSQSVSTSHSYMHYQQRPGQPPKLLIKYASNL	60
		: : : : : : : : :	
QY	61	GYPARFSGSGSTDTFLNIHPVEEDASTYYCOHSGELPPTFGSGPKLEIK	111
		: : : : : : : : :	
Db	61	GYPARFSGSGSTDTFLNIHPVEEDATYYCOHSGEIPYTFGGGPKLEIK	111
		: : : : : : : : :	

RESULT 15
US-08-653-402B-12
; Sequence 12, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millien, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/653,402B
 FILING DATE: 24-MAY-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95107967.2
 FILING DATE: 26-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lebovitz, Richard M.
 REGISTRATION NUMBER: 37,067
 REFERENCE/DOCKET NUMBER: MERCK 1781
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-653-402B-12

		Query Match	84.7%;	Score	489.5;	DB 2;	Length	146;	
		Best Local Similarity	87.4%;	Pred.	No. 1.5e-44;				
		Matches	97;	Conservative	5;	Mismatches	8;	Gaps	1;
QY	1	DIVLTQPASLAVSLGQRATISCRASKSVSAGSYNMYHWOOKAQGPKLJIHLASNLES	60						
Db	21	DIVLTQPASLAVSLGQRATISYRASKSVSTGYSYMHWNOKQPQLLIYLVSNLES	80						
QY	61	GVPARFSGSGSGTDTLINIHVPEEDASTYYCQHSGELPFTFGSGTKLEIK	111						
Db	81	GVPARFSGSGSGTDTLINIHVPEEDASTYYCOHIREV-YTFGGGTKEIK	130						

Search completed: June 28, 2001, 16:01:15
Job time: 523 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:45 ; Search time 234.85 Seconds
(without alignments)
36.003 Million cell updates/sec

Title: US-09-724-406-26
Perfect score: 578
Sequence: 1 DIVLTQSPASLAVSLGQRAT.....CQHSGELPFTFGSGTKLEIK 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	92.7	111	1 KVM575	Ig kappa chain V r
2	534	92.4	111	1 KVM584	Ig kappa chain V r
3	528	91.3	111	1 KVM540	Ig kappa chain V r
4	524	90.7	210	2 A56169	Ig kappa chain V r
5	524	90.7	218	2 JC5810	monoclonal antibod
6	520	90.0	112	2 S45715	Ig kappa chain V r
7	520	90.0	218	2 S68241	Ig kappa chain V r
8	517	89.4	111	1 KVM585	Ig kappa chain V r
9	509	88.1	131	2 S55027	Ig kappa chain V r
10	507	87.7	111	2 S09963	Ig light chain pre
11	493	85.3	111	1 KVM543	Ig kappa chain V-J
12	490	84.8	108	1 KVM554	Ig kappa chain V r
13	488	84.4	111	1 KVM508	Ig kappa chain V r
14	486.5	84.2	110	2 S24288	Ig kappa chain V r
15	486	84.1	140	2 PN0466	Ig kappa chain pre
16	482	83.4	111	1 KVM583	Ig kappa chain V r
17	482	83.4	111	1 KVM593	Ig kappa chain V r
18	479	82.9	112	2 S19972	Ig kappa chain V r
19	476	82.4	102	2 PH1077	Ig light chain V r
20	475	82.2	111	1 KVM5C1	Ig kappa chain V r
21	473.5	81.9	110	1 KVM510	Ig kappa chain V r
22	473	81.8	112	2 S19976	Ig kappa chain V r
23	471.5	81.6	108	2 PH0092	Ig kappa chain V r
24	469.5	81.2	233	2 JC5322	p53 specific singl
25	468	81.0	112	2 S19971	Ig kappa chain V r
26	468	81.0	131	2 PH1226	Ig kappa chain pre
27	466	80.6	102	2 PH1076	Ig light chain V r
28	461	79.8	101	2 S59640	Ig light chain V r
29	459	79.4	111	1 KVM537	Ig kappa chain V r

ALIGNMENTS

RESULT 1

KVM575

Ig kappa chain V region (PC7175) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000

C:Accession: B01938; A01938

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Accession: B01938

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 92.7%; Score 536; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 1.6e-41;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGVNYHWHYQKAGQPPKLLIHLASNLES 60

Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVTSVSGSYHWHYQKPGQPPKLLIYLASNLES 60

Qy 61 GVPARFSGSGSTDTFTLNHPVEEEDASTYYCQHSGLPFTFGSGTKLEIK 111

Db 61 GVPARFSGSGSTDTFTLNHPVEEEDASTYYCQHSRLPFTFGAGTKLEK 111

RESULT 2

KVM584

Ig kappa chain V region (PC6684) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000

C:Accession: A01938

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152

A:Accession: A01938

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

```

30 459 79.4 115 2 S63596 Ig kappa chain V r
31 458 79.2 131 1 KVM5M6 Ig kappa chain pre
32 448 77.5 111 2 PL0081 Ig kappa chain V r
33 446.5 77.2 102 2 PC6027 acetylcoline recep
34 446 77.2 111 1 KVM580 Ig kappa chain V r
35 446 77.2 111 1 KVM550 Ig kappa chain V r
36 446 77.2 128 2 S52448 Ig kappa chain V r
37 446 77.2 128 2 JL0073 aberrant kappa tra
38 444 76.8 111 2 D45722 anti-glycoprotein
39 441 76.3 111 2 S09969 Ig kappa chain V-J
40 441 76.3 111 2 E53285 Ig kappa chain V a
41 440 76.1 111 2 S09966 Ig kappa chain V-J
42 439 76.0 107 2 S26343 Ig kappa chain V r
43 437 75.6 132 1 KVM532 Ig kappa chain pre
44 436 75.4 111 2 S09965 Ig kappa chain V-J
45 434 75.1 109 2 PH0093 Ig kappa chain V r

```

F;23-92/Disulfide bonds: #status predicted

Query Match 92.4%; Score 534; DB 1; Length 111;
 Best Local Similarity 92.8%; Pred. No. 2.4e-41;
 Matches 103; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 3
 KVM540
 Ig kappa chain V region (PC7940) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
 C:Accession: C01938; A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: C01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 91.3%; Score 528; DB 1; Length 111;
 Best Local Similarity 92.8%; Pred. No. 8.4e-41;
 Matches 103; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 4
 A56169
 Ig kappa chain V region (clone 23.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
 C:Accession: A56169
 R:Monfardini, C.; Kleber-Emmons, T.; VonFelddt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
 J. Biol. Chem. 270, 6628-6638, 1995
 A:Title: Recombinant antibodies in bioactive peptide design.
 A:Reference number: A56169; MUID:95204454
 A:Accession: A56169
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-210 <MON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 90.7%; Score 524; DB 2; Length 210;
 Best Local Similarity 89.2%; Pred. No. 3.8e-40;
 Matches 99; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60

DB 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60
 QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 5
 JC5810
 monoclonal antibody 13-1 light chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
 C:Accession: JC5810
 R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
 A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
 A:Reference number: JC5810; MUID:98063277
 A:Accession: JC5810
 A:Molecule type: protein
 A:Residues: 1-218 <AKA>
 C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 524; DB 2; Length 218;
 Best Local Similarity 91.0%; Pred. No. 3.9e-40;
 Matches 101; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60
 DB 1 NIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 6
 S45715
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
 C:Accession: S45715
 R:Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, FEBS Lett. 346, 246-250, 1994
 A:Title: Application of ¹³C NMR spectroscopy to paratope mapping for larger antigen
 A:Reference number: S45714; MUID:94283606
 A:Accession: S45715
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-112 <KIM>
 A:Experimental source: cell line EX-3C7
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 90.0%; Score 520; DB 2; Length 112;
 Best Local Similarity 88.3%; Pred. No. 4.5e-40;
 Matches 98; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60
 DB 1 DIVLTQSPASLAVSLGORATISCRASKSVSGYNYMHVYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 61 GVPARFSGSGGDTFTLNHPVEEDASTYYCOHSGELPFTFGSGTKLEIK 111

RESULT 7

823071
 S68241
 Ig kappa chain V region (Mab13-1) - mouse (fragment)
 N:Alternate names: immunoglobulin light chain
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S68241; S68214
 R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
 Submitted to the EMBL Data Library, March 1994
 A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
 A:Reference number: S68241
 A:Accession: S68241
 A:Molecule type: mRNA
 A:Residues: 1-218 <TAK>
 A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
 R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
 FEBS Lett. 375, 273-276, 1995
 A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
 A:Reference number: S68211; MUID:96085223
 A:Accession: S68214
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 'NI',3-212 <TAK>
 A:Cross-references: EMBL:D29670
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

	Query Match	90.0%	Score 520;	DB 2;	Length 218;
	Best Local Similarity	89.2%;	Pred. No. 9e-40;		
	Matches	99;	Conservative	6;	Mismatches
				6;	Indels
				0;	Gaps
QY	1	DIVLTQSPASLAVSLGQRATISCRASKSVSASGYIMHWYQKAGQPPKLLIHLASNL	60		
		:::			
Db	1	EVLVTQSPASLAVSLGQRATISCRASKSVSASGYIMHWYQKPGQPPKLLISLATNL	60		
QY	61	GVPARFSGSGSGTFTLNHPVEEDASTYYCQHSGLPFTFGSGTKLEIK	111		
Db	61	GVPARFSGSGSGTFTLNHPVEEDVATYQHSRELPLTFTGAGTKLEIK	111		

```

RESULT      8
KWS85
Ig kappa chain V regions (PC2485, PC4039) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
C:Accession: A01939
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: A01939
A:Molecule type: protein
A:Residues: 1-111 <WEI>
A:Note: the PC2485 and PC4039 sequences are identical
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate in C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

```

	Query Match	89.4%	Score 517;	DB 1;	Length 111;
	Best Local Similarity	89.2%	Prod. No. 8.2e-40;		
	Matches 99;	Conservative	6;	Mismatches 26;	
				Indels	0; Gaps 0;
QY	1	DIVLTQSPASLVSLGORATISCRASKYSVASGYNMHWYQKAGOPKLLIHLSNLES	60		
Ddb	1	DIVLTQSPASLVSLGORATISCRASKSVSTGISTMHWYQKAGOPKLLIYIASSLES	60		
QY	61	GVPARFSGSGGTDFTLTIHNPVEEDASTSYVQHSGLPFTFGSGTKLEIK	111		

db 61 GVPARFSGSGTDFTLNIQPVVEEDAAIYYCQHSRELPLTFGAGTKLELK 111

```

RESULT      9
S55027
Ig light chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: S55027
R:Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff, J. Mol. Biol. 248, 344-360, 1995
A:Title: Structure and specificity of the anti-digoxin antibody 40-50.
A:Reference number: S55027; MUID:95257394
A:Accession: S55027
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <JEFF>
A:Cross-references: EMBL:L31404; NID:g476719; PIDN:AAA72437.1; PID:g476720
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-114/Domain: immunoglobulin homology <IMM>

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```

Query Match      88.1%; Score 509; DB 2; Length 131;
Best Local Similarity 87.4%; pred. No. 5.1e-39;
Matches 97; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      1 DIVLTQSPASIAVSLGQRATISCRASKSVASGYNYMHWTQQRAGQPPKLLIHLASNLFS 60
|||||
Db      21 DIVLTQSPASIAVSLGQRATISCRASKSVSTSGYSHIHWYQQRGPPKLLIYLASILEFS 80
|||||

QY      61 GVPARFSGSGGCTDFTLNIHPVEEDASTYYCQHSGLPPTFGSGTKLEIK 111
|||||
Db      81 GVPARFSGSGGCTDFTLNIHPVEEDASTYYCQHSREYPLTFGAGTELEIK 131
|||||

```

```

RESULT 10
S09963
Ig kappa chain V-J region (103-7E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09963
C:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibio
A:Reference number: S09955; MUID:90269328
A:Accession: S09963
A:Molecule type: mRNA
A:Residues: 1-111 <REI>
A:Cross-references: EMBL:X51851
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

```

Query Match	87.7%	Score 507;	DB 2;	Length 111;		
Best Local Similarity	86.5%;	pred. No. 6.5e+39;				
Matches	96;	Conservative	7; Mismatches	8; Indels	0; Gaps	0;
QY	1	DIVLTQSPASLAVSGQRATISCRASKSVASGSYNMYHQKAGOPPKLLIHLSANLES	60			
Db	1	DIVLTQSPASLAVSLGRATLSRASQSVSSGYSYMHYQKQPGSPKLLIKYASNLES	60			
QY	61	GYPARFSGSGGTDTFLNIHPVEEDASTYYCOHSGELPTFGSGYKLEIK	111			
Db	61	GYPARFSGSGGTDTFLNIHPVEEDATYYCOHSEIPTYTFGGYKLEIK	111			

RESULT 11
KYMS43
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01940
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: A01940
A:Molecule type: protein
A:Residues: 1-108 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a heterotrimer.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 84.8%; Score 490; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 2.1e-37;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNLES 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 DIVLAQSPASLTVSLGQRATISCRASQSVTSGYNMHWYQKPGQPPKLLIKYASNLES 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 61 GVPARFSGSGGTDFTLNIHPVEEDASTYCYQHSGLPFTFGSGTKL 108
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 GVPARFSGSGGTDFTLNIHPVEEDAAAYICQHSWEIPLTFGAGTKL 108
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 13
KVMS08
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: C01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a heterotrimer.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 84.4%; Score 488; DB 1; Length 111;
Best Local Similarity 84.7%; Pred. No. 3.3e-37;
Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNLES 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 DIVLTQSPASLAVSLGQRATISCRASQSVTDGDSYMWYQKPGQPPKLLIYTASNLES 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 61 GVPARFSGSGGTDFTLNIHPVEEDASTYCYQHSGLPFTFGSGTKLEIK 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 GIPARFSGSGGTDFTLNIHPVEEDAAITYCQSNEDPWTFGSGTKLEIK 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 14
S24288
Ig kappa chain V region (JS28/32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S24288
R:Monchamont, B.
submitted to the EMBL Data Library, September 1991
A:Description: Cloning and sequencing of the cDNA coding for the variable regions of
A:Reference number: S24287

A:Accession: S24288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <MON>
A:Cross-references: EMBL:X62703; NID:G51673; PIDN:CAA44576.1; PID:gl333958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 486.5; DB 2; Length 110;
Best Local Similarity 86.5%; Pred. No. 4.5e-37;
Matches 96; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVSYSGYNYMHYQKAGQPPKLLIHLASNL 60

DB 1 DIQLTQSPASLAVSLGQRATISYRASKSVSYSGYNYMHYQKAGQPPKLLIHLASNL 60

QY 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGELPFTFGSGTKLEIK 111

DB 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHIRE-PYTFGGTKLEIK 110

RESULT 15

PN0446

Ig kappa chain precursor V-II region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0446

R:Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera

A:Reference number: PN0444; MUID:93138402

A:Accession: PN0446

A:Molecule type: mRNA

A:Residues: 1-140 <KAL>

A:Cross-references: GB:L02345

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-140/Product: Ig light chain kappa-2 V region #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 486; DB 2; Length 140;
Best Local Similarity 87.4%; Pred. No. 6.4e-37;
Matches 97; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVSYSGYNYMHYQKAGQPPKLLIHLASNL 60

DB 21 DIVLTQSPASLAVSLGQRATISYRASKSVSYSGYNYMHYQKAGQPPKLLIHLASNL 80

QY 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGELPFTFGSGTKLEIK 111

DB 81 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHIREL--TFGGTKLEIK 129

Search completed: June 28, 2001, 15:58:46
Job time: 374 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:38 ; Search time 105.36 Seconds
(without alignments)
36.089 Million cell updates/sec

Title: US-09-724-406-26

Sequence: 578
1 DIVLTQSPASLAVSLGQRAT.....COHSGELPFTFGSGTKLEIK 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	92.7	111	1	KV3S_MOUSE
2	534	92.4	111	1	KV3R_MOUSE
3	528	91.3	111	1	KV3T_MOUSE
4	517	89.4	111	1	KV3U_MOUSE
5	493	85.3	111	1	KV3M_MOUSE
6	490	84.8	108	1	KV3V_MOUSE
7	488	84.4	111	1	KV3O_MOUSE
8	482	83.4	111	1	KV3N_MOUSE
9	482	83.4	111	1	KV3Q_MOUSE
10	475	82.2	111	1	KV3L_MOUSE
11	473.5	81.9	110	1	KV3P_MOUSE
12	460	79.6	111	1	KV3J_MOUSE
13	459	79.4	111	1	KV3H_MOUSE
14	458	79.2	131	1	KV3I_MOUSE
15	456	78.9	111	1	KV3K_MOUSE
16	452	78.2	111	1	KV3C_MOUSE
17	446	77.2	111	1	KV3A_MOUSE
18	446	77.2	111	1	KV3D_MOUSE
19	437.5	75.7	112	1	KV3B_MOUSE
20	437	75.6	132	1	KV3E_MOUSE
21	433	74.9	112	1	KV3G_MOUSE
22	418	72.3	111	1	KV3E_MOUSE
23	385	66.6	134	1	KV4C_HUMAN
24	383	66.3	114	1	KV4A_HUMAN
25	374.5	64.8	133	1	KV4B_HUMAN
26	369	63.8	108	1	KV5P_MOUSE
27	359	62.1	129	1	KV1W_HUMAN
28	352.5	61.0	129	1	KV3L_HUMAN
29	351.5	60.8	129	1	KV3M_HUMAN
30	350.5	60.6	109	1	KV3D_HUMAN
31	349.5	60.5	113	1	KV2G_MOUSE
32	349.5	60.5	129	1	KV4A_MOUSE
33	347	60.0	108	1	KV1B_HUMAN

34 347 60.0 108 1 KVIY_HUMAN P80362 homo sapien
35 346.5 59.9 109 1 KV3E_HUMAN P01623 homo sapien
36 346.5 59.9 113 1 KV2E_MOUSE P03976 mus musculus
37 345.5 59.8 112 1 KV2D_MOUSE P01629 mus musculus
38 345 59.7 108 1 KVIY_HUMAN P04430 homo sapien
39 344.5 59.6 117 1 KV2E_HUMAN P06309 homo sapien
40 343.5 59.4 109 1 KV3B_HUMAN P01620 homo sapien
41 342.5 59.3 113 1 KV2D_HUMAN P01617 homo sapien
42 342.5 59.3 129 1 KV3H_HUMAN P04207 homo sapien
43 342 59.2 108 1 KVIH_HUMAN P01600 homo sapien
44 342 59.2 108 1 KVIK_HUMAN P01603 homo sapien
45 342 59.2 108 1 KVIW_HUMAN P01605 homo sapien

ALIGNMENTS

RESULT 1
KV3S_MOUSE
ID KV3S_MOUSE STANDARD: PRT: 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: B01938; KVM575.
DR InterPro: IPR003006;
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 92.7%; Score 536; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 8.5e-48;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNHWHYQKAGQPPKLLIHLASNL 60
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVTSVSGSYHWHYQKAGQPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDTLNHPVEEDASTYVCOHSGELPFTFGSGTKLEIK 111
Db 61 GVPARFSGSGGTDTLNHPVEEDASTYVCOHSGELPFTFGSGTKLEIK 111

RESULT 2
KV3R_MOUSE
ID KV3R_MOUSE STANDARD: PRT: 111 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6584.

THE

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01937; KVM543.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 85.3%; Score 493; DB 1; Length 111;
 Best Local Similarity 85.6%; Pred. No. 1.9e-43;
 Matches 95; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 Db 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 QY 61 GVPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKLEIK 111
 Db 61 GIPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKLEIK 111

RESULT 6
 KV3V_MOUSE
 ID KV3V_MOUSE STANDARD; PRT; 108 AA.
 AC P01674;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 2154.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01940; KVM54.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 108
 FT DISULFID 23 92
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;

Query Match 84.8%; Score 490; DB 1; Length 108;
 Best Local Similarity 86.1%; Pred. No. 3.8e-43;
 Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 Db 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 QY 61 GVPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKL 108
 Db 61 GVPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKL 108

RESULT 7
 KV3O_MOUSE
 ID KV3O_MOUSE STANDARD; PRT; 111 AA.
 AC P01667;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 6308.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: C01937; KVM508.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 84.4%; Score 488; DB 1; Length 111;
 Best Local Similarity 84.7%; Pred. No. 6.3e-43;
 Matches 94; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 Db 1 DIVLTQSPASLAVSLGORATISCRASKSVASGYNMHWYQKAGOPPKLLIHLASNL 60
 QY 61 GVPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKLEIK 111
 Db 61 GIPARFSGSGTDFTLNHPVEEDASTYCYQHSGELPFTFGSGTKLEIK 111

RESULT 8
 KV3N_MOUSE
 ID KV3N_MOUSE STANDARD; PRT; 111 AA.
 AC P01666;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 7183.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity";
 RL Nature 276:785-790(1978).
 DR PIR; B01937; KVM583.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111
 FT FRAMEWORK 4.
 FT BY SIMILARITY.
 FT DISULFID 23 92
 FT NON_TER 111
 FT SEQUENCE 111 AA; 2058BB50CE306D31 CRC64;

Query Match 83.4%; Score 482; DB 1; Length 111;
 Best Local Similarity 82.9%; Pred. No. 2.5e-42;
 Matches 92; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||
 Db 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||

Qy 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGSGTKLEIK 111
 |:
 Db 61 GIPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGAGTKLEIK 111
 |:
 RESULT 9
 KV3Q_MOUSE STANDARD; PRT; 111 AA.
 ID KV3Q_MOUSE
 AC P01669;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 7769.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity";
 RL Nature 276:785-790(1978).
 DR PIR; B01937; KVM583.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111
 FT FRAMEWORK 4.
 FT BY SIMILARITY.
 FT DISULFID 23 92
 FT NON_TER 111
 FT SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 83.4%; Score 482; DB 1; Length 111;

Best Local Similarity 83.8%; Pred. No. 2.5e-42;
 Matches 93; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||
 Db 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||

Qy 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGSGTKLEIK 111
 |:
 Db 61 GIPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGSGTKLEIK 111
 |:
 RESULT 10
 KV3L_MOUSE STANDARD; PRT; 111 AA.
 ID KV3L_MOUSE
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CBPC 101.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -I- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR; A01936; KVM581.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53
 FT FRAMEWORK 2.
 FT DOMAIN 54 60
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92
 FT FRAMEWORK 3.
 FT DOMAIN 93 101
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111
 FT FRAMEWORK 4.
 FT BY SIMILARITY.
 FT NON_TER 111
 FT SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 82.2%; Score 475; DB 1; Length 111;
 Best Local Similarity 82.0%; Pred. No. 1.3e-41;
 Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||
 Db 1 DIVLTQSPASVLSLQGRATISCRASKSVASGYNYMHVYQKAGQPPKLLIHLASNLDES 60
 |||||

Qy 61 GVPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGSGTKLEIK 111
 |:
 Db 61 GIPARFSGSGGTDFTLNHPVEEEDASTYCYQHSGLPFTFGSGTKLEIK 111
 |:
 RESULT 11
 KV3P_MOUSE STANDARD; PRT; 110 AA.
 ID KV3P_MOUSE
 AC P01668;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 7210.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

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RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL Nature 276:785-790(1978).
DR PIR; D01937; KWS10.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 29 53
FT DOMAIN 34 60
FT DOMAIN 39 92
FT DOMAIN 44 100
FT DOMAIN 49 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 81.9%; Score 473.5; DB 1; Length 110;
Best Local Similarity 82.9%; Pred. No. 1.8e-41;
Matches 92; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
Db 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
Db 61 GIPARFSGSGGTDFLTNIHPVEEDASTYYC-HQSEDPTFGSGTKLEIK 110

RESULT 12
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KWSM6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 44 60
FT DOMAIN 49 92
FT DOMAIN 54 101
FT DOMAIN 59 101
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 81.9%; Score 473.5; DB 1; Length 110;
Best Local Similarity 82.9%; Pred. No. 1.8e-41;
Matches 92; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
Db 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
Db 61 GIPARFSGSGGTDFLTNIHPVEEDASTYYC-HQSEDPTFGSGTKLEIK 110

RESULT 12
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KWSM6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 44 60
FT DOMAIN 49 92
FT DOMAIN 54 101
FT DOMAIN 59 101
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

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FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 79.6%; Score 460; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 4.3e-40;
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
Db 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
Db 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111

RESULT 13
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KWS37.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 44 60
FT DOMAIN 49 92
FT DOMAIN 54 101
FT DOMAIN 59 101
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 79.4%; Score 459; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 5.5e-40;
Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
Db 1 DIVLTQSPASVSLGQRATISCRASKSVASGYNMHWYQQKAGPPKLLIHLASNL 60
QY 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111
Db 61 GVPARFSGSGGTDFLTNIHPVEEDASTYYCQHSGLPFTFGSGTKLEIK 111

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RESULT 14

KV31_MOUSE STANDARD; PRT; 131 AA.
 AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=78235887; PubMed=98179;
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 the variable and constant regions of immunoglobulin light chain
 precursors: implications on the organization and controlled
 expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-131.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 kappa chains with limited sequence differences.";
 RL Biochemistry 12:760-771(1973).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR PIR; A01935; KVM56.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 79.2%; Score 458; DB 1; Length 131;
 Best Local Similarity 80.2%; Pred. No. 8.3e-40;
 Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRTATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 21 NVLTQSPASLAVSLGQRTATISCRASEVDSYGNFPMHWYQKAGQPPKLLIHLASNL 80
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 GVPARFSGSGGTDFTLTNPVPEEDASTYCYQHSGELPFTFGSGTKLEIK 111
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 81 GVPARFSGSGSRDFTLTIDPVEADDAATYCYQCNNEPFTFGGKLEIK 131

RESULT 15

KV3K_MOUSE STANDARD; PRT; 111 AA.
 ID KV3K_MOUSE
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR; A01935; KVM56.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38 FRAMEWORK 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 78.9%; Score 456; DB 1; Length 111;
 Best Local Similarity 79.3%; Pred. No. 1.1e-39;
 Matches 88; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIVLTQSPASLAVSLGQRTATISCRASKSVASGYNMHWYQKAGQPPKLLIHLASNL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 NVLTQSPASLAVSLGQRTATISCRASEVDSYGNFPMHWYQKAGQPPKLLIHLASNL 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 GVPARFSGSGGTDFTLTNPVPEEDASTYCYQHSGELPFTFGSGTKLEIK 111
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 GVPARFSGSGSRDFTLTIDPVEADDAATYCYQCNNEPFTFGAGTKLEIK 111

Search completed: June 28, 2001, 15:54:39
 Job time: 127 sec

Fri Jun 29 08:04:57 2001

us-09-724-406-26.rsp

Page 7

69 SGGTDFTLNIHPVEEDASTYYCQHSGELPTFFGGTKLEIK 111
 |||||:|||||: :||| :||| :|||
 61 SGGTDFSNIHPVEEDIAMFCQQRKKVPWTFGGTKLEIK 103

OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	'Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	tissue.';	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
CC	DOMAIN.	
DR	EMBL: AF035031; RAD56267.1; -.	
DR	HSSP: P01607; 1RET	
DR	InterPro: IPR003006; -.	
DR	InterPro: IPR003596; -.	
DR	Pfam: PF00047; Ig; 1.	
DR	SMART: SM00406; IGV; 1.	
FT	NON_TER 1	
FT	NON_TER 108	
FT	NON_TER 108	
FT	NON_TER 11834 MW: 9F9C5A92F8A96FA CBCEA.	
SQ	SEQUENCE 108 AA: 11834 MW: 9F9C5A92F8A96FA CBCEA.	

	Query Match	61.4%	Score 355;	DB 4;	Length 108;
	Best Local Similarity	61.3%;	Pred. No. 1.4e-31;		
	Matches	68;	Conservative	20;	Mismatches 19; Indels 4; Gaps 1;
QY	1	DIVLTQSPTASLAVSGQRATISCRASKSVASGNYMHYYQQKAGOPKKLLIHLSNLES	60		
	:	: :			
Db	1	EIVMTQSPATLSVSPERATISCRASQSVSSN----	LAWYQQKPGQAPRLIIYCASTRAT	56	
QY	61	GYPARFSGSGSTDTFLNIHVPEEDASTYYCQHSGELPFTFCGGTKLEIK	111		
	:	: :			
Db	57	GIPARFSGSGSGETFLIRISQLLEDFAVICQHNWNPETFGPGTKVDIK	107		

[illegible]

Query Match 59.48; Score 343.5; DB 4; Length 107;
Best Local Similarity 60.48; Pred. No. 2.5e-30;

	Matches	67;	Conservative	20;	Mismatches	19;	Indels	5;	Gaps	2
QY	1	DIVLTQSPASLAVSLGQRATISCRASKSVASGYNMHWYQQKAGOPPKLLIHLSANLES	60							
		: : : - : : : - : : :								
Db	1	DIQMTPSSPSSLASVGDRTVITCRASQSIS----	NLYNWYQKPCKAPNLLIIAASSLOS	56						
QY	61	GVPAFSGSGGTDTFLNIHPVEEDASTYYCOHSGELPFTFGSGTKLEIK	111							
		: : : : : : : : : :								
Db	57	GVPSRFGSGSGTDTFLTISGLQAEDFATYYCQSYS-ALTEGPCTKVDIR	106							
RESULT	7									
Q9UL79										
ID	Q9UL79		PRELIMINARY;	PRT;	108 AA.					
AC	Q9UL79;									
DT	01-MAY-2000	(TriEMBLrel. 13, Created)								
DT	01-MAY-2000	(TriEMBLrel. 13, Last sequence update)								
DE	01-MAR-2001	(TriEMBLrel. 16, Last annotation update)								
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).									
OS	Homo sapiens (Human).									
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
OX	NCBI_TaxID=9606;									
RN	[1]									

[illegible]

Query Match	59.3%	Score 343;	DB 4;	Length 108;
Best Local Similarity	60.4%;	Pred. No. 2.8e-30;		
Matches	67;	Conservative 16;	Mismatches 24;	Indels 4; Gaps 1;
Qy	1	DIVVTQSPASIAVSLGORATISCRASKSVSASGYNMHVYQQKAGQPPKLLIHLASNL	60	
		: : : : : : : : : : : : : : : :		
Db	1	DIVVTQSPSLLSASTGRVITISCRMSQGIS---SYLAWYQKPKAPELLIIYAASTLQS	56	
Qy	61	GVPAFFSGSGGTDFTLNIHPVEEDASTYCOHSGELPPTFFSGSGTKLEIK	111	
		: : : : : : : : : : : : : : :		
Db	57	GVPRFSGSGSGTDFTLTISLGDSERATYCCQYVYFPPTFFGGCTKVEIK	107	

RESULT	8
Q90YF0	
ID	Q90YF0 PRELIMINARY; PRT; 298 AA.
AC	Q90YF0;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	CN 8 SCFV.
DN	CN 8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei
QC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C; TISSUE=SPLEEN;

RA Shinohara N., Demura T., Fukuda H.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RA Shinohara N., Demura T., Fukuda H.;
 RT "Isolation of a novel type of vascular cell wall-specific monoclonal
 RT antibody recognizing a cell polarity using a phase display subtraction
 RT method.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB036341; BAA88633.1; -
 DR HSP; P01607; IREI.
 DR InterPro: IPR003006; -
 DR InterPro: IPR003596; -
 DR Pfam: PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 58.3%; Score 337; DB 11; Length 298;
 Best Local Similarity 56.8%; Pred. No. 4.3e-29;
 Matches 63; Conservative 20; Mismatches 24; Indels 4; Gaps 1;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNYMHYQKAGQPPKLLIHLASNLSES 60
 DB 173 DIELTQSPASLSASVGETVITTCRASGNI----HNYLAWYQKQKSPQLLYVNAKTLAD 228

QY 61 GVPARFSGSGCTDFTLNHPVEEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 229 GVPFRSGSGGTQYSLKINSLOPEDFGSYCYQHFWTPTFTGGGKLEIK 279

RESULT 9
 QYERZ9 PRELIMINARY; PRT; 107 AA.
 AC QYERZ9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
 RT "Cloning and sequencing of the light chain fragment of variable region
 RT genes of an anti-hTNF-a monoclonal antibody.";
 RL J. Cell. Mol. Immunol. 12:21-26(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
 RT "Construction and sequencing of the single-chain antibody gene of a
 RT human TNF-alpha specific monoclonal antibody.";
 RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF262753; AAG23804.1; -
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 57.4%; Score 332; DB 11; Length 107;
 Best Local Similarity 59.8%; Pred. No. 4.5e-29;
 Matches 64; Conservative 18; Mismatches 23; Indels 2; Gaps 1;

QY 4 LTQSPASLAVSLGQRATISCRASKSV--SASGYNYMHYQKAGQPPKLLIHLASNLSESG 61
 DB 1 MTQSPSSLSAMSVGKVTMSCKSSQSLNSNTQKRYLAWYQKQSPQLLYVFASTREG 60

QY 62 VPARFSGSGCTDFTLNHPVEEEDASTYYCOHSGELPFTFGSGTKL 108
 DB 61 VPDREMGSGCTDFTLTISSVQTEDLADYFCQHQHYRTPFTFGSGTKL 107

RESULT 10
 QYERZ9 PRELIMINARY; PRT; 109 AA.
 AC QYERZ9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035028; AAD56264.1; -
 DR HSP; P01789; IMCP.
 DR InterPro: IPR003006; -
 DR InterPro: IPR003596; -
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 57.2%; Score 330.5; DB 4; Length 109;
 Best Local Similarity 59.5%; Pred. No. 6.8e-29;
 Matches 66; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKSVASGYNYMHYQKAGQPPKLLIHLASNLSES 60
 DB 1 EIVLTQSPGTLSLFPGERATISCRASQSVSS--YLAWYQKQPGAPRLIYGTSSRAT 57

QY 61 GVPARFSGSGCTDFTLNHPVEEEDASTYYCOHSGELPFTFGSGTKLEIK 111
 DB 58 GIPDRFSGSGSETDFTLTISRLEPEDFAVYICQYQYSSIFTPGPKVDIK 108

RESULT 11
 QYERZ9 PRELIMINARY; PRT; 214 AA.
 AC QYERZ9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv)."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152371; AAD40242.1; -
 DR HSP; P01789; IMCP.
 DR InterPro: IPR003006; -

Best Local Similarity 59.3%; Pred. No. 2.2e-28;
Matches 67; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKS-VSASGYNMYHYYQQKAGQPPKLLIHLASNLE 59
Db 1 DVWMTQSPATLSVSPGERATLSCWASQSISSN---LANVYQKPGQAPRLIIYGASTRAT 60
QY 60 SGVPARESGSGGTDFTLNHPVEEEDASTYYC-OHSGELPFTFGSGTKLEIK 111
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYCMQGTTHWPPFTFGGQTKVEIK 113

RESULT 15

Q9UL85 PRELIMINARY; PRT; 109 AA.
AC OSUL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF035029; AAD56265.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 55.4%; Score 320.5; DB 4; Length 109;
Best Local Similarity 57.1%; Pred. No. 8.5e-28;
Matches 64; Conservative 23; Mismatches 20; Indels 5; Gaps 2;

QY 1 DIVLTQSPASLAVSLGQRATISCRASKS-VSASGYNMYHYYQQKAGQPPKLLIHLASNLE 60
Db 1 EIVMTQSPATLSVSPGERATLSCWASQSISSN---LANVYQKPGQAPRLIIYGASTRAT 56
QY 61 GVPARESGSGGTDFTLNHPVEEEDASTYYC-OHSGELPFTFGSGTKLEIK 111
Db 57 GIPARESGSGGTEFTLTISLSQSEDFAIYHCQQYNSWPPLTFGGQTKVEIK 108

Search completed: June 28, 2001, 16:08:26
Job time: 954 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:38 ; Search time 362.28 Seconds
(without alignments)
2.510 Million cell updates/sec

Title: US-09-724-406-28

Perfect score: 77

Sequence: 1 RASKSVASGYNVYM 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

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- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
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- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	94.8	151	22	Antibody variable
2	72	93.5	110	15	Anti-carcinoembryo
3	72	93.5	110	20	Murine COL1 VK cha
4	72	93.5	110	20	Humanised Murine C
5	72	93.5	110	20	Humanised Murine C
6	72	93.5	110	20	Humanised Murine C
7	72	93.5	110	20	Humanised Murine C
8	68	88.3	16	16	Humanised Murine C
9	68	88.3	98	19	L-CDR-1 of anti-id
10	68	88.3	108	12	Light chain of mon
11	68	88.3	110	16	Murine IB4 light c
					Immunoglobulin lig

12	68	88.3	110	16	Immunoglobulin lig
13	68	88.3	110	17	285 light chain va
14	68	88.3	110	18	Monoclonal antibod
15	68	88.3	110	20	Protein sequence o
16	68	88.3	110	20	Protein sequence o
17	68	88.3	110	20	Murine 340 VI amin
18	68	88.3	110	21	317G5 hybridoma VL
19	68	88.3	112	11	N-terminal sequenc
20	68	88.3	124	12	Light chain variab
21	68	88.3	128	17	HNK-20 variable ka
22	68	88.3	130	16	Anti-idiotypic anti
23	68	88.3	131	13	p12-k2. Synthetic
24	68	88.3	146	16	Anti-idiotypic anti
25	68	88.3	146	18	Mouse anti-idiotyp
26	68	88.3	212	15	Porphylin antibody
27	64	83.1	15	21	H. pylori HSP60-b1
28	64	83.1	111	21	H. pylori HSP60-b1
29	61	79.2	111	13	Humanised VL regio
30	61	79.2	111	13	Light chain variab
31	61	79.2	111	22	Murine Fd79 antibo
32	61	79.2	111	22	Humanised Fd79 ant
33	60	77.9	22	16	GM-CSF receptor al
34	59	76.6	111	17	Humanised antibody
35	59	76.6	111	17	Murine 206 antibody
36	59	76.6	112	16	Human thyroid stim
37	57	74.0	17	19	CDR1 of the light
38	56	72.7	15	16	Mouse antibody var
39	56	72.7	437	19	Nucleotide sequenc
40	54	70.1	112	16	VL region from an
41	52	67.5	125	12	Light chain variab
42	48	62.3	132	17	Anti-human gp39 MA
43	44	57.1	15	16	Mouse antibody var
44	44	57.1	218	16	Mouse antibody FB3
45	44	57.1	218	16	Mouse antibody F4-

ALIGNMENTS

RESULT 1
ID AAB35100 standard; Protein; 151 AA.
AC AAB35100;
DT 27-MAR-2001 (first entry)
DE Antibody variable region fusion protein #4.
KW Filamentous phage; protein display; pVII; pIX;
KW combinatorial antibody library.
OS Synthetic.
PN WO200071694-A1.
PD 30-NOV-2000.
PF 24-MAY-2000; 2000WO-US14433.
PR 25-MAY-1999; 99US-0318786.
PX (SCRI) SCRIPPS RES INST.
PA Janda KD, Wirsching P, Lerner RA, Gao C;
PI WPI; 2001-032030/04.
PT Novel filamentous phage encapsulating a genome encoding fusion
PT polypeptide comprising exogenous polypeptide fused to amino terminus of
PT pVII and pIX proteins, for constructing diverse heterodimeric
PT polypeptide array

PS Example 1; Page 82-83; 90pp; English.

CC The present invention describes a filamentous phage encapsulating a
CC genome encoding a fusion protein. This fusion protein comprises an
CC exogenous protein fused to the amino terminus of a filamentous phage pVII
CC or pIX protein. This is useful in the design of proteins for medical,
CC industrial, environmental and research applications.

XX Sequence 151 AA;

Query Match 94.8%; Score 73; DB 22; Length 151;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RAKSVSASGYNM 15
DB 24 rasksvstsgynmh 38
|||||

RESULT 2

AA60564
ID AAR60564 standard; Protein; 110 AA.

XX

AC AAR60564;

XX 25-APR-1995 (first entry)

DT Anti-carcinoembryonic antigen chimeric light chain Ab.

DE Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW chimeric human-murine; breast or colorectal carcinoma;
KW light chain.

XX Chimeric Mus muscaris.

OS Chimeric Homo sapiens.

XX WO9419466-A.

XX 01-SEP-1994.

XX 16-FEB-1994; 94WO-US01709.

XX 16-FEB-1993; 93US-0017570.

XX (DOWC) DOW CHEM CO.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Gourlie BB, Kaplan DA, Mezes PS, Rixon MW, Schlom J;

XX WPI; 1994-294331/36.

XX N-PSDB; AAQ71394.

XX Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis
XX and therapy of carcinoma, e.g. breast or colorectal carcinoma
XX Claim 11; Page 50; 67pp; English.

XX AAQ71394 codes for AAR60564 the antibody light chain region of
XX murine-human anti-carcinoembryonic antigen (CEA) chimeric
XX antibody. Which can be used in in vitro immunoassays for
XX the detection of CEA, and monitoring of tumour-associated
XX antigen during therapy. It can also be used in vivo diagnostically,
XX or in therapy for the treatment of tumours associated with
XX colorectal and breast carcinomas, as well those of the
XX gastrointestinal tract, lung, ovary and pancreas.

XX Sequence 110 AA;

Query Match 93.5%; Score 72; DB 15; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAKSVSASGYNM 15
DB 24 rasksvsagsysmh 38
|||||

RESULT 3

AA39532
ID AAY39532 standard; protein; 110 AA.

XX AAY39532;

XX 22-NOV-1999 (first entry)

DE Murine COL1 VK chain (COL1MuVK).

XX Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX Mus sp.

XX WO9943817-A1.

XX 02-SEP-1999.

XX 25-FEB-1998; 98WO-US03680.

XX 25-FEB-1998; 98WO-US03680.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;

XX WPI; 1999-550870/46.

XX New antibody specific for treatment and diagnosis of cancer -
XX Claim 2; Fig 2; 82pp; English.

XX This sequence represents the murine COL1 VK chain (COL1MuVK), and was
XX used to obtain the humanised antibody (Ab) of the invention. The
XX humanised Ab, or its fragment, specifically binds to carcinoembryonic
XX antigen (CEA). The Ab, optionally coupled to an effector or label, is
XX used to treat or prevent CEA-expressing cancers (e.g. of breast, ovary,
XX lung, stomach, or colon) and to detect CEA-expressing cells, either in
XX vitro (optionally on a solid support) or in vivo (particularly by tumour
XX imaging to identify tumours and metastases before surgery), for diagnosis
XX or prognosis. It is not significantly immunogenic, i.e. the Ab does not
XX induce a human anti-murine antibody or allergic response, or non-specific
XX cytotoxicity, so can be administered repeatedly. It retains specificity
XX for CEA, and has improved clearance (allowing efficient targeting) and
XX metabolic properties.

XX Sequence 110 AA;

Query Match 93.5%; Score 72; DB 20; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAKSVSASGYNM 15
DB 24 rasksvsagsysmh 38
|||||

RESULT 4

AA39534
ID AAY39534 standard; protein; 110 AA.

XX AAY39534;

XX 22-NOV-1999 (first entry)

XX

```

DE Humanised Murine COL1 VK chain (COL1REVK).
XX
KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9943817-A1.
XX
PD 02-SEP-1999.
XX
PF 25-FEB-1998; 98WO-US03680.
XX
PR 25-FEB-1998; 98WO-US03680.
XX
PX 25-FEB-1998; 98WO-US03680.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 1999-550870/46.
XX
PT New antibody specific for treatment and diagnosis of cancer -
XX
PS Claim 2; Fig 2; 82pp; English.
XX
CC This sequence represents a humanised version of the murine COL1 VK chain,
CC designated COL1REVK, and was used to obtain the humanised antibody (Ab)
CC of the invention. The humanised Ab, or its fragment, specifically binds
CC to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an
CC effector or label, is used to treat or prevent CEA-expressing cancers
CC (e.g. of breast, ovary, lung, stomach, or colon) and to detect
CC CEA-expressing cells, either in vitro (optionally on a solid support) or
CC in vivo (particularly by tumour imaging to identify tumours and
CC metastases before surgery), for diagnosis or prognosis. It is not
CC significantly immunogenic, i.e. the Ab does not induce a human
CC anti-murine antibody or allergic response, or non-specific cytotoxicity,
CC so can be administered repeatedly. It retains specificity for CEA, and
CC has improved clearance (allowing efficient targeting) and metabolic
CC properties.
XX
SQ Sequence 110 AA;

Query Match 93.5%; Score 72; DB 20; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15
Db 24 RASKSVSASGYSYMH 38
|||||:|||||:|||||

RESULT 5
AAY39535
ID AAY39535 standard; protein; 110 AA.
XX
AC AAY39535;
XX
DT 22-NOV-1999 (first entry)
XX
DE Humanised Murine COL1 VK chain (COL1REVK).
XX
KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 3

Humanised Murine COL1 VK chain (COL1REVK).
XX
KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9943817-A1.
XX
PD 02-SEP-1999.
XX
PF 25-FEB-1998; 98WO-US03680.
XX
PR 25-FEB-1998; 98WO-US03680.
XX
PX 25-FEB-1998; 98WO-US03680.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 1999-550870/46.
XX
PT New antibody specific for treatment and diagnosis of cancer -
XX
PS Claim 2; Fig 2; 82pp; English.
XX
CC This sequence represents a humanised version of the murine COL1 VK chain,
CC designated COL1REVK, and was used to obtain the humanised antibody (Ab)
CC of the invention. The humanised Ab, or its fragment, specifically binds
CC to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an
CC effector or label, is used to treat or prevent CEA-expressing cancers
CC (e.g. of breast, ovary, lung, stomach, or colon) and to detect
CC CEA-expressing cells, either in vitro (optionally on a solid support) or
CC in vivo (particularly by tumour imaging to identify tumours and
CC metastases before surgery), for diagnosis or prognosis. It is not
CC significantly immunogenic, i.e. the Ab does not induce a human
CC anti-murine antibody or allergic response, or non-specific cytotoxicity,
CC so can be administered repeatedly. It retains specificity for CEA, and
CC has improved clearance (allowing efficient targeting) and metabolic
CC properties.
XX
SQ Sequence 110 AA;

Query Match 93.5%; Score 72; DB 20; Length 110;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15
Db 24 RASKSVSASGYSYMH 38
|||||:|||||:|||||

RESULT 6
AAY39544
ID AAY39544 standard; protein; 110 AA.
XX
AC AAY39544;
XX
DT 22-NOV-1999 (first entry)
XX
DE Humanised Murine COL1 VK chain variant COL1VK HuVKF.
XX
KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9943817-A1.
XX
PD 02-SEP-1999.
XX

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PF 25-FEB-1998; 98WO-US03680.
 XX
 PR 25-FEB-1998; 98WO-US03680.
 XX
 PA (DOWC) DOW CHEM CO.
 XX
 PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
 XX
 DR WPI; 1999-550870/46.
 XX
 PT New antibody specific for treatment and diagnosis of cancer
 PS
 PS Disclosure; Page 44; 82pp; English.
 XX
 CC This sequence is a humanised variant version of the murine COL1 VK chain,
 CC designated COL1NMVK, and was used to obtain the humanised antibody (Ab)
 CC of the invention. The humanised Ab, or its fragment, specifically binds
 CC to carcinoembryonic antigen (CEA). The Ab, optionally coupled to an
 CC effector or label, is used to treat or prevent CEA-expressing cancers
 CC (e.g. of breast, ovary, lung, stomach, or colon) and to detect
 CC CEA-expressing cells, either in vitro (optionally on a solid support) or
 CC in vivo (particularly by tumour imaging to identify tumours and
 CC metastases before surgery), for diagnosis or prognosis. It is not
 CC significantly immunogenic, i.e. the Ab does not induce a human
 CC anti-murine antibody or allergic response, or non-specific cytotoxicity,
 CC so can be administered repeatedly. It retains specificity for CEA, and
 CC has improved clearance (allowing efficient targeting) and metabolic
 CC properties.
 XX
 SQ Sequence 110 AA;
 Query Match 93.5%; Score 72; DB 20; Length 110;
 Best Local Similarity 93.3%; Pred. No. 1.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASKSVASGYNM 15
 DB 24 rasksvasgysymh 38
 |||||
 RESULT 8
 AAR74945
 ID AAR74945 standard; peptide; 16 AA.
 XX
 AC AAR74945;
 XX
 DT 19-JAN-1996 (first entry)
 XX
 DE L-CDR-1 of anti-idiotypic antibody against human anticancer antibody.
 XX
 KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 XX JP07101999-A.
 XX
 PD 18-APR-1995.
 XX
 PF 06-OCT-1993; 93JP-0272950.
 XX
 PR 06-OCT-1993; 93JP-0272950.
 XX
 PA (HAGI/) HAGIWARA Y.
 XX
 DR WPI; 1995-182987/24.
 XX
 XX Novel anti-idiotypic antibody against a human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX
 PS Claim 11; Page 4; 28pp; Japanese.
 XX
 CC A new anti-idiotypic antibody against a human anticancer monoclonal
 CC antibody is claimed. This antibody contains in its heavy chain 3
 CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2
 CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
 CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
 CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
 CC encoding it are useful in pharmacological, medical and biochemical
 CC fields.
 XX
 SQ Sequence 16 AA;
 Query Match 93.5%; Score 72; DB 20; Length 110;
 Best Local Similarity 93.3%; Pred. No. 1.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASKSVASGYNM 15
 DB 24 rasksvasgysymh 38
 |||||
 RESULT 7
 AAY39546
 ID AAY39546 standard; protein; 110 AA.
 XX
 AC AAY39546;
 XX
 DT 22-NOV-1999 (first entry)
 XX
 DE Humanised Murine COL1 VK chain variant.
 XX
 KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
 KW tumour identification; metastasis; diagnosis; mouse; VK chain.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9943817-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 25-FEB-1998; 98WO-US03680.
 XX
 PR 25-FEB-1998; 98WO-US03680.
 XX
 PA (DOWC) DOW CHEM CO.
 XX
 PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
 XX
 DR WPI; 1999-550870/46.
 XX
 PT New antibody specific for treatment and diagnosis of cancer
 PS

Query Match 88.3%; Score 68; DB 16; Length 16;
 Best Local Similarity 86.7%; Pred. No. 6.8e-06;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15
 ||||| |||:|
 DB 2 rasksvstsgysymh 16

RESULT 9

AAW70952
 ID AAW70952 standard; protein; 98 AA.

AC AAW70952;

DT 14-OCT-1998 (first entry)

DE Light chain of monoclonal antibody RS-2B8.

XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
 KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
 KW viral infection; inhibit; fusion; protection; transcription;
 KW antiviral agent; prophylaxis; diagnosis; infection; contamination.

XX Mus sp.

XX FR2758331-A1.

PN 17-JUL-1998.

PF 14-JAN-1997; 97FR-0000300.

PR 14-JAN-1997; 97FR-0000300.

XX (UYBO-) UNIV BOURGOGNE.

XX Bourgeois C, Kohl E, Pothier P;

XX WPI; 1998-390320/34.

XX New peptide(s) recognising viral epitope with tropism to mucosa -
 PT useful for, e.g. diagnosing, preventing and treating viral
 PT infection(s)

PS Disclosure; Fig 2; 51pp; French.

XX The present sequence represents the light chain of monoclonal antibody
 CC RS-2B8, which is directed against the respiratory syncytial virus (RSV).
 CC The specification describes peptides which recognise, by
 CC antigen-antibody type reactions, at least 1 epitope of a pathogenic virus
 CC having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous
 CC to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are
 CC analogous to CDR regions of monoclonal antibodies specific for site III
 CC or IV of the VP6 protein of rota virus (RV). The peptides can neutralise
 CC viral infections and may also inhibit fusion between infected and
 CC uninfected cells or cells and viruses. They provide passive or active
 CC protection and/or inhibit transcription of the virus, so are useful as
 CC antiviral agents or for prophylaxis, in human or veterinary medicine. The
 CC peptides can be labelled and used to diagnose infection or contamination
 CC by the virus. The peptides are particularly directed against RSV or RS
 CC but may also be used against papilloma, adeno, entero, polio, influenza
 CC or immune deficiency viruses.

XX Sequence 98 AA;

Query Match 88.3%; Score 68; DB 19; Length 98;
 Best Local Similarity 86.7%; Pred. No. 5.6e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15

DB 15 rasksvstsgysymh 29
 ||||| |||:|

RESULT 10

AAAR13088
 ID AAR13088 standard; Protein; 108 AA.

XX AAR13088;

XX 01-OCT-1991 (first entry)

XX Murine 1B4 light chain-1 variable region.

XX Monoclonal antibody; complementarity determining region; CDR;
 KW integrin; hybridoma 1B4; protein REI; Gal/Rei; Ig.

XX EP438312-A.

PN EP440351-A.

XX 24-JUL-1991.

XX 17-JAN-1991; 91EP-0300367.

XX 20-DEC-1990; 90US-0627421.

PR 19-JAN-1990; 90US-0467692.

XX (MERI) MERCK & CO INC.

XX Law MF, Mark GE, Schmidt JA, Singer II;

XX WPI; 1991-216985/30.

DR N-PSDB; AAQ12683.

XX New recombinant immunoglobulin(s) reactive with leukocyte CD18
 PT antigen - comprise human heavy chain framework and murine
 PT complementarity regions useful in treatment of inflammation

XX Disclosure; Fig 24; 77pp; English.

XX A recombinant human Ig comprises a human heavy chain framework
 CC and murine CDRs (with the heavy chain framework mutated at sites
 CC near the CDRs), a human light chain framework and murine CDRs.
 CC It has a mean IC50 nearly equal to that of the murine monoclonal
 CC antibody from which the CDRs were derived. It is designated
 CC mutated Gal/Rei. The human Ig is capable of binding to a human
 CC CD18 integrin.

CC The murine CDRs are obtd. from murine hybridoma 1B4

CC (ATCC HB 10164). The light chain framework is derived from

CC human myeloma protein REI (EP-239400).

CC See also AAQ12682-84.

XX Sequence 108 AA;

Query Match 88.3%; Score 68; DB 12; Length 108;
 Best Local Similarity 86.7%; Pred. No. 6.3e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15

DB 24 rasksvstsgysymh 38

RESULT 11

AAAR74956
 ID AAR74956 standard; Protein; 110 AA.

XX AAR74956;

XX 19-JAN-1996 (first entry)

XX Immunoglobulin light chain of anti-idiotypic antibody against human

DE anticancer antibody.
 XX
 KW Antibody; cancer; CDR: heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN JP07101999-A.
 XX
 XX
 PD 18-APR-1995.
 XX
 XX 06-OCT-1993; 93JP-0272950.
 XX
 XX 06-OCT-1993; 93JP-0272950.
 XX
 PA (HAGI/) HAGIWARA Y.
 XX
 XX WPI; 1995-182987/24.
 DR N-PSDB; AAQ90421.
 XX
 XX Novel anti-idiotype antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 PS
 PS Claim 13; Page 4; 28pp; Japanese.

CC AAR74955-R74959 are possible light chains of a new anti-idiotype
 CC antibody against a human anticancer monoclonal antibody. This antibody
 CC contains in its heavy chain 3 complementarity determining regions CDR1
 CC (AAR74929-R74931), CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),
 CC this is also true of the light chain which has its own CDR1
 CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
 CC (AAR74950-R74954). The antibody and DNA encoding it are useful in
 CC pharmacological, medical and biochemical fields.
 XX
 XX Sequence 110 AA;

Query Match 88.3%; Score 68; DB 16; Length 110;
 Best Local Similarity 86.7%; Pred. No. 6.4e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15
 DB 24 rasksvstsgysmh 38
 ||||| |||:|

RESULT 12

AAR74957
 ID AAR74957 standard; Protein; 110 AA.

XX
 AC AAR74957;

XX 22-JAN-1996 (first entry)

XX Immunoglobulin light chain of anti-idiotype antibody against human
 DE anticancer antibody.

XX Antibody; cancer; CDR: heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.

XX Mus sp.

XX JP07101999-A.

XX 18-APR-1995.

XX 06-OCT-1993; 93JP-0272950.

XX 06-OCT-1993; 93JP-0272950.

XX (HAGI/) HAGIWARA Y.

XX

DR WPI; 1995-182987/24.
 DR N-PSDB; AAQ90423.
 XX
 XX Novel anti-idiotype antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX
 XX Claim 14; Page 4; 28pp; Japanese.
 XX
 CC AAR74955-R74959 are possible light chains of a new anti-idiotype
 CC antibody against a human anticancer monoclonal antibody. This antibody
 CC contains in its heavy chain 3 complementarity determining regions CDR1
 CC (AAR74929-R74931), CDR2 (AAR74932-R74935) and CDR3 (AAR74936-R74939),
 CC this is also true of the light chain which has its own CDR1
 CC (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3
 CC (AAR74950-R74954). The antibody and DNA encoding it are useful in
 CC pharmacological, medical and biochemical fields.
 XX
 XX Sequence 110 AA;

Query Match 88.3%; Score 68; DB 16; Length 110;
 Best Local Similarity 86.7%; Pred. No. 6.4e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNM 15

DB 24 rasksvstsgysmh 38
 ||||| |||:|

RESULT 13

AAR90832

ID AAR90832 standard; Protein; 110 AA.

XX AAR90832;

XX 25-JUN-1996 (first entry)

XX 2B5 light chain variable region from pCIB4616.

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;

KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
 KW antibody.

XX Insecta sp.

XX WO9600783-A1.

XX 11-JAN-1996.

XX 20-JUN-1995; 95WO-IB00497.

XX 28-JUN-1994; 94US-0267641.

XX (CIBA) CIBA GEIGY AG.

XX Carozzi NB, Koziel MG;

XX WPI; 1996-077494/08.
 DR N-PSDB; AAT15728.

XX New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants

XX Claim 8; Page 57; 106pp; English.

XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;
 CC isolating immunocompetent B cells from the immunised animal; fusing B
 CC cells with a tumour cell line; isolating the fused cells, culturing them
 CC and cloning positive hybrid cells; and screening the hybrid cells for

CC prodn. of the required MABs. The MABs bind to the gut of a target insect
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
 CC Pseudomonas exotoxin and phytoalexin, etc.. The Abs are useful for
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
 CC maize.
 XX
 SQ Sequence 110 AA;

Query Match 88.3%; Score 68; DB 17; Length 110;
 Best Local Similarity 86.7%; Pred. No. 6.4e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNVHM 15
 ||||| |||||
 Db 24 rasksvstsgsynh 38

RESULT 14

AAW22952
 ID AAW22952 standard; Protein; 110 AA.

XX
 AC AAW22952;

XX
 DT 02-APR-1998 (first entry)

XX
 DE Monoclonal antibody (MAB) 340 light chain variable region.

XX
 KW MAB 340; monoclonal antibody; foetal cell; pre-natal diagnosis;
 KW erythrocyte; trophoblast; genetic abnormality; foetal sex; analysis;
 KW epidermal growth factor receptor; EGFR; Down's syndrome; human.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH Region 1..23
 FT Region /note= "Framework 1"
 FT Region 24..38
 FT Region /note= "Complementarity-determining region 1"
 FT Region 39..53
 FT Region /note= "Framework 2"
 FT Region 54..60
 FT Region /note= "Complementarity-determining region 2"
 FT Region 61..92
 FT Region /note= "Framework 3"
 FT Region 93..100
 FT Region /note= "Complementarity-determining region 3"
 FT Region 101..110
 FT Region /note= "Framework 4"

XX W09730354-A2.

XX
 PD 21-AUG-1997.

XX
 PF 17-FEB-1997; 97WO-GB00443.

XX
 PR 16-FEB-1996; 96GB-0003249.

XX (UYNO-) UNIV NOTTINGHAM.

XX Durrant LG, Liu DT;

XX
 PI WPI; 1997-425169/39.

XX
 DR N-PSDB; AAT75584.

XX
 PT Foetal cell analysis comprising isolating at least 2 sorts of foetal
 PT cell from maternal sample - specifically nucleated red cells and
 PT trophoblasts, useful for pre-natal diagnosis of genetic
 PT abnormalities or foetal sex
 XX
 PS Example 2; Page 15; 31pp; English.

XX

CC This is the light chain variable region of a monoclonal antibody (MAB)
 CC 340. The MAB 340 acts as a trophoblast binding agent in a method for
 CC analysing human foetal cells. The method comprises isolating at least 2
 CC types of nucleated foetal cell from a maternal sample. The foetal cells
 CC specifically are nucleated red cells (erythrocytes) and trophoblasts.
 CC The trophoblasts are isolated by contacting the maternal sample with a
 CC specific binding agent that binds to the epidermal growth factor receptor
 CC (EGFR). MAB340 or an EGFR binding derivative of MAB340 comprising at
 CC least the CDR regions of one or other of the light or heavy chain
 CC variable regions of MAB 340 is used as the binding agent. Erythrocytes
 CC are also isolated with a specific anti-transferrin antibody. The target
 CC nucleotide sequences in the foetal cells are amplified by PCR primers.
 CC The isolated cells can be used for genetic and biochemical analysis,
 CC particularly to determine the sex of the foetus or to detect inherited
 CC abnormalities, e.g. Down's syndrome. More generally MAB 340 can be used
 CC to enrich (for subsequent analysis) rare malignant cells, e.g. squamous
 CC carcinoma cells, that express EGF receptor. The method is not
 CC significantly invasive and does not carry the risk of inducing abortion.
 CC Use of two types of cells significantly improves the sensitivity of
 CC pre-natal diagnosis.
 XX
 SQ Sequence 110 AA;

Query Match 88.3%; Score 68; DB 18; Length 110;

Best Local Similarity 86.7%; Pred. No. 6.4e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNVHM 15

||||| |||||

Db 24 rasksvstsgsynh 38

RESULT 15

AAW86123

ID AAW86123 standard; Protein; 110 AA.

XX
 AC AAW86123;

XX
 DT 03-MAR-1999 (first entry)

XX Protein sequence of de-immunised 340 vl.

XX Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunoglobulin; therapeutic; streptokinase; de-immunised.

XX Homo sapiens.

XX W09852976-A1.

XX
 PD 26-NOV-1998.

XX
 PF 21-MAY-1998; 98WO-GB01473.

XX
 PR 14-APR-1998; 98GB-0007751.

XX
 PR 21-MAY-1997; 97GB-0010480.

XX
 PR 31-JUL-1997; 97GB-0016197.

XX
 PR 28-NOV-1997; 97GB-0025270.

XX
 PR 02-DEC-1997; 97US-0067235.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ;

XX
 DR WPI; 1999-045301/04.

XX Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 XX

PS Example 1; Fig 5; 77pp; English.

XX

CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised 340 Vh.
 XX
 SQ Sequence 110 AA;

Query Match 88.3%; Score 68; DB 20; Length 110;
 Best Local Similarity 86.7%; Pred. No. 6.4e-05;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVASAGYNYMH 15
 Db 24 rasksvstsgysymh 38

Search completed: June 28, 2001, 16:14:38
 Job time: 1326 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:15 ; Search time 138.34 Seconds
(without alignments)
2.184 Million cell updates/sec

Title: US-09-724-406-28
Perfect score: 77
Sequence: 1 RASKSVSAGSYNYMH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	93.5	110	1	US-08-017-570-2
2	72	93.5	110	1	US-08-471-426-2
3	72	93.5	110	5	PCT-US94-01709-2
4	69	89.6	20	2	US-08-712-212-1
5	69	89.6	20	5	PCT-US95-05160-1
6	68	88.3	15	1	US-08-137-117D-136
7	68	88.3	15	2	US-08-436-717-136
8	68	88.3	16	1	US-08-318-970B-13
9	68	88.3	110	3	US-08-442-542-8
10	68	88.3	110	3	US-08-483-749A-20
11	68	88.3	110	3	US-08-765-469-8
12	68	88.3	130	1	US-08-137-117D-86
13	68	88.3	130	2	US-08-436-717-86
14	68	88.3	131	1	US-08-137-117D-25
15	68	88.3	131	2	US-08-436-717-25
16	68	88.3	146	2	US-08-653-402B-12
17	61	79.2	111	1	US-07-634-278-46
18	61	79.2	111	1	US-07-634-278-47
19	61	79.2	111	1	US-08-477-728-46
20	61	79.2	111	1	US-08-477-728-47
21	61	79.2	111	1	US-08-207-169A-4
22	61	79.2	111	1	US-08-474-040-46
23	61	79.2	111	1	US-08-474-040-47
24	61	79.2	111	1	US-08-487-200-46
25	61	79.2	111	1	US-08-487-200-47
26	61	79.2	111	4	US-08-484-537-46
27	61	79.2	111	4	US-08-484-537-47

28	60	77.9	128	5	PCT-US95-15716-6	Sequence 6, Appl
29	56	72.7	111	5	PCT-US94-14106-53	Sequence 53, Appl
30	48	62.3	132	2	US-08-379-057-16	Sequence 16, Appl
31	44	57.1	218	5	PCT-US94-14106-57	Sequence 57, Appl
32	42	54.5	111	1	US-08-111-080-30	Sequence 30, Appl
33	42	54.5	111	1	US-08-111-080-32	Sequence 32, Appl
34	42	54.5	111	1	US-08-275-053-11	Sequence 11, Appl
35	42	54.5	111	1	US-08-275-053-14	Sequence 14, Appl
36	42	54.5	111	1	US-08-211-980-30	Sequence 30, Appl
37	42	54.5	111	1	US-08-211-980-32	Sequence 32, Appl
38	42	54.5	111	5	PCT-US93-07967-30	Sequence 30, Appl
39	42	54.5	111	5	PCT-US93-07967-32	Sequence 32, Appl
40	42	54.5	121	1	US-08-111-080-18	Sequence 18, Appl
41	42	54.5	121	1	US-08-111-080-22	Sequence 22, Appl
42	42	54.5	121	1	US-08-211-980-18	Sequence 18, Appl
43	42	54.5	121	1	US-08-211-980-22	Sequence 22, Appl
44	42	54.5	121	5	PCT-US92-07111-17	Sequence 17, Appl
45	42	54.5	121	5	PCT-US93-07967-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-017-570-2
; Sequence 2, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-017-570-2

Query Match 93.5%; Score 72: DB 1; Length 110;
Best Local Similarity 93.3%; Pred. No. 3.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKSVSAGSYNYMH 15
|||||||

Db 24 RASKSVSASGYSYMH 38

RESULT 2

US-08-471-426-2

Sequence 2, Application us/08471426

Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/017,570

FILING DATE: 16-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-426-2

Query Match 93.5%; Score 72; DB 1; Length 110;

Best Local Similarity 93.3%; Pred. No. 3.5e-05;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYSYMH 15

Db 24 RASKSVSASGYSYMH 38

RESULT 3

PCT-US94-01709-2

Sequence 2, Application PC/TUS9401709

Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: THE DOW CHEMICAL COMPANY

APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01709

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: 38,777-F

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-01709-2

Query Match 93.5%; Score 72; DB 5; Length 110;

Best Local Similarity 93.3%; Pred. No. 3.5e-05;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYSYMH 15

Db 24 RASKSVSASGYSYMH 38

RESULT 4

US-08-712-212-1

Sequence 1, Application US/08712212

Patent No. 5837460

GENERAL INFORMATION:

APPLICANT: Williams, William V.

APPLICANT: Kieber-Emmons, Thomas

APPLICANT: Weiner, David B.

APPLICANT: Vonfeldt, Joan M.

TITLE OF INVENTION: Biologically active peptides and

TITLE OF INVENTION: methods of identifying the same

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: No. 5837460is

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/712,212

FILING DATE: 03-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,404

FILING DATE: 29-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: UPN-1554

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-712-212-1

Query Match 89.6%; Score 69; DB 5; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
|||||:|||||

DB 2 RASKSVSSSGYSYMH 16

RESULT 5

PCT-US95-05160-1
Sequence 1, Application PC/TUS9505160
GENERAL INFORMATION:
APPLICANT: Williams, William V.
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Weiner, David B.
APPLICANT: Vonfeldt, Joan M.
TITLE OF INVENTION: Biologically active peptides and
TITLE OF INVENTION: methods of identifying the same
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05160
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,404
FILING DATE: 29-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2245
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05160-1

Query Match 89.6%; Score 69; DB 5; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.7e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
|||||:|||||

DB 2 RASKSVSSSGYSYMH 16

RESULT 6

US-08-137-117D-136
Sequence 136, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALJANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 136:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-137-117D-136

Query Match 88.3%; Score 68; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.9e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15

DB 1 RASKSVSTSGISYMH 15

RESULT 7

US-08-436-717-136
Sequence 136, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 24-APR-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-136

Query Match 88.3%; Score 68; DB 2; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.9e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
Db 1 RASKSVSTSGYSYMH 15

RESULT 8
US-08-318-970B-13
Sequence 13, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: Hideaki HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street

CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: L CDR1-2
OTHER INFORMATION: hypervariable region
US-08-318-970B-13

Query Match 88.3%; Score 68; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
Db 2 RASKSVSTSGYSYMH 16

RESULT 9
US-08-442-542-8
Sequence 8, Application US/08442542
Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Kozziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: CGC 1750
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-542-8

Query Match 88.3%; Score 68; DB 1; Length 110;
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15
Db 24 RASKSVSTSGYSYM 38

RESULT 10

US-08-483-749A-20
Sequence 20, Application US/08483749A
Patent No. 6054561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-20

Query Match 88.3%; Score 68; DB 3; Length 110;
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15
Db 24 RASKSVSTSGYSYM 38

RESULT 11

US-08-765-469-8
Sequence 8, Application US/08765469
Patent No. 6069301
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Kozziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-469-8

Query Match 88.3%; Score 68; DB 3; Length 110;
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15
Db 24 RASKSVSTSGYSYM 38

RESULT 12

US-08-137-117D-86
Sequence 86, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-86

Query Match 88.3%; Score 68; DB 1; Length 130;
Best Local Similarity 86.7%; Pred. No. 0.00019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNMH 15
||||||| |||:||||
DB 43 RASKSVSTSGYSYMH 57

RESULT 13
US-08-436-717-86
Sequence 86, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-86

Query Match 88.3%; Score 68; DB 2; Length 130;
Best Local Similarity 86.7%; Pred. No. 0.00019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNMH 15
||||||| |||:||||
DB 43 RASKSVSTSGYSYMH 57

RESULT 14
US-08-137-117D-25
Sequence 25, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/126/AAOK
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904135
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-137-117D-25

Query Match 88.3%; Score 68; DB 1; Length 131;
 Best Local Similarity 86.7%; Pred. No. 0.00019;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
 ||||| |||:
 Db 44 RASKSVSTSGYSYMH 58

RESULT 15

US-08-436-717-25
 Sequence 25, Application US/08436717
 Patent No. 5817790

GENERAL INFORMATION:
 APPLICANT: TSUCHIYA, Masayuki
 APPLICANT: SATO, Koh
 APPLICANT: BENDIG, Mary
 APPLICANT: JONES, Steven
 APPLICANT: SALDANHA, Jose
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
 NUMBER OF SEQUENCES: 158
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436.717
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/137.117
 FILING DATE: 20-DEC-1993
 APPLICATION NUMBER: WO PCT/JP92/00544
 FILING DATE: 24-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 4-32084
 FILING DATE: 19-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 3-95476
 FILING DATE: 25-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WEGNER, Harold C.
 REGISTRATION NUMBER: 25,258
 REFERENCE/DOCKET NUMBER: 53466/126/AAOK
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904135
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-436-717-25

Query Match 88.3%; Score 68; DB 2; Length 131;
 Best Local Similarity 86.7%; Pred. No. 0.00019;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
 ||||| |||:
 Db 44 RASKSVSTSGYSYMH 58

Search completed: June 28, 2001, 16:01:15
 Job time: 523 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:46 ; Search time 234.85 Seconds
(without alignments)
4.865 Million cell updates/sec

Title: US-09-724-406-28
Perfect score: 77
Sequence: 1 RASKSVSASGYNM 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	69	89.6	210	2 A56169	Ig kappa chain v r
2	68	88.3	102	2 PC6027	acetylcoline recep
3	68	88.3	108	2 PH0092	Ig kappa chain v r
4	68	88.3	110	2 S24288	Ig kappa chain v r
5	68	88.3	111	1 KVM584	Ig kappa chain v r
6	68	88.3	111	1 KVM575	Ig kappa chain v r
7	68	88.3	111	1 KVM585	Ig kappa chain v r
8	68	88.3	112	2 S45715	Ig kappa chain v r
9	68	88.3	128	2 S52448	Ig kappa chain v r
10	68	88.3	128	2 JL0073	aberrant kappa tra
11	68	88.3	140	2 PN0446	Ig kappa chain pre
12	68	88.3	218	2 S68241	Ig kappa chain v r
13	68	88.3	218	2 JC5810	monoclonal antibod
14	68	88.3	233	2 JC5322	p53 specific singl
15	66	85.7	111	1 KVM5A0	Ig kappa chain v r
16	65	84.4	111	2 S09563	Ig kappa chain v r
17	64	83.1	108	1 KVM5S4	Ig kappa chain v r
18	59	76.6	131	2 S55027	Ig kappa chain v r
19	58	75.3	102	2 PH1076	Ig light chain pre
20	54	70.1	102	2 PH1077	Ig light chain v r
21	53	68.8	101	2 S59640	Ig light chain v r
22	52	67.5	115	2 S63596	Ig kappa chain v r
23	43	55.8	109	2 PH0093	Ig kappa chain v r
24	42	54.5	91	2 S25462	Ig kappa chain v r
25	42	54.5	107	2 S26343	Ig kappa chain v r
26	42	54.5	107	2 S26344	Ig kappa chain v r
27	42	54.5	111	1 KVM537	Ig kappa chain v r
28	42	54.5	111	2 D45722	anti-glycoprotein
29	42	54.5	131	1 KVM5M6	Ig kappa chain pre

30 42 54.5 764 2 T48446
31 41 53.2 111 2 E53285
32 41 53.2 112 2 S19972
33 41 53.2 221 2 A56941
34 41 53.2 233 2 T01233
35 41 53.2 301 2 B61164
36 41 53.2 608 2 B53295
37 41 53.2 2693 2 A40743
38 40 51.9 320 1 A39479
39 40 51.9 321 1 S28390
40 40 51.9 346 2 T20458
41 40 51.9 662 2 B75544
42 39 50.6 112 2 S51122
43 38.5 50.0 94 2 PL0258
44 38 49.4 96 2 S17608
45 38 49.4 96 2 B49442

ALIGNMENTS

RESULT 1
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God J. Biol. Chem. 270, 5628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
A;Accession: A56169
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.6%; Score 69; DB 2; Length 210;
Best Local Similarity 86.7%; Pred. No. 0.00013;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNM 15
DB 24 RASKSVSSSGSYMH 38
RESULT 2
PC6027
acetylcoline receptor monoclonal antibody A7 light chain variable region - mouse (fra
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jan-2000
C;Accession: PC6027
R;Meng, F.; Yang, K.; Graus, Y.; de Baets, M.
Chinese J. Microbiol. Immunol. 16, 45-48, 1996
A;Title: Pathogenicity and sequence analysis of a mouse anti-AChR monoclonal antibody
A;Reference number: PC6026
A;Accession: PC6027
A;Molecule type: mRNA
A;Residues: 1-102 <MEN>
A;Cross-references: EMBL:X80961
C;Comment: This protein induces acetylcoline receptor loss and muscular weakness in m
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;8-86/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 102;
Best Local Similarity 86.7%; Pred. No. 9.1e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNM 15
||||||| |||||

Db 16 RASKSVSTSGSYMH 30

RESULT 3

Ig kappa chain V region (anti-cyclosporin F) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
 C:Accession: PH0092
 R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koher, H.P.; Quesniaux, V.F.J.; V
 Mol. Immunol. 27, 1029-1038, 1990
 A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
 A:Reference number: PH0087; MUID:91042649
 A:Accession: PH0092
 A:Molecule type: mRNA
 A:Residues: 1-108 <SCH>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:24-38/Region: complementarity-determining 1
 F:54-60/Region: complementarity-determining 2
 F:93-100/Region: complementarity-determining 3

Query Match 88.3%; Score 68; DB 2; Length 108;

Best Local Similarity 86.7%; Pred. No. 9.6e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15

||||| |||:|

Db 24 RASKSVSTSGSYMH 38

RESULT 4

Ig kappa chain V region (J528/32) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
 C:Accession: S24288
 R:Moncharmont, B.
 submitted to the EMBL Data Library, September 1991
 A:Description: Cloning and sequencing of the cDNA coding for the variable regions of the
 A:Reference number: S24287
 A:Accession: S24288
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-110 <MON>
 A:Cross-references: EMBL:X62703; NID:951673; PIDN:CAA44576.1; PID:g1333958
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 110;

Best Local Similarity 86.7%; Pred. No. 9.8e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15

||||| |||:|

Db 24 RASKSVSTSGSYMH 38

RESULT 5

Ig kappa chain V region (PC6684) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
 C:Accession: A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01938

A:Molecule type: protein

A:Residues: 1-111 <WEI>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 88.3%; Score 68; DB 1; Length 111;

Best Local Similarity 86.7%; Pred. No. 9.9e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15

||||| |||:|

Db 24 RASKSVSTSGSYMH 38

RESULT 6

Ig kappa chain V region (PC7175) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
 C:Accession: B01938; A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 88.3%; Score 68; DB 1; Length 111;

Best Local Similarity 86.7%; Pred. No. 9.9e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKSVSASGYNM 15

||||| |||:|

Db 24 RASKSVSTSGSYMH 38

RESULT 7

Ig kappa chain V regions (PC2485, PC4039) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
 C:Accession: A01939
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01939
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 A:Note: the PC4285 and PC4039 sequences are identical
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 88.3%; Score 68; DB 1; Length 111;

Best Local Similarity 86.7%; Pred. No. 9.9e-05;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
||||||| |||:|

Db 24 RASKSVSTSGYSYMH 38

RESULT 8

Ig kappa chain V region - mouse (fragment)
S45715

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999

C:Accession: S45715

R:Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A.

FEB5 Lett. 346, 246-250, 1994

A:Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen-Pa

A:Reference number: S45714; MUID:94283606

A:Accession: S45715

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-112 <KIM>

A:Experimental source: cell line Ex-3C7

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

F:23-92/Disulfide bonds: #status predicted

Query Match 88.3%; Score 68; DB 2; Length 112;

Best Local Similarity 86.7%; Pred. No. 0.0001;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15

||||||| |||:|

Db 24 RASKSVSTSGYSYMH 38

RESULT 9

S52448

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S52448

R:Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A:Description: Specific amplification by the polymerase chain reaction of rearranged ge

A:Reference number: S52445

A:Accession: S52448

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-128 <BER>

A:Cross-references: EMBL:X82689

C:Genetics:

A:Introns: 14/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-115/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 128;

Best Local Similarity 86.7%; Pred. No. 0.00011;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15

||||||| |||:|

Db 45 RASKSVSTSGYSYMH 59

RESULT 10

JL0073

aberrant kappa transcript - mouse

C:Species: Mus musculus (house mouse)

C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000

C:Accession: JL0073

R:Carroll, W.L.; Mendel, E.; Levy, S.

Mol. Immunol. 25, 991-995, 1988

A:Title: Hybridoma fusion cell lines contain an aberrant kappa transcript.

A:Reference number: JL0073; MUID:89112230

A:Accession: JL0073

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <CAR>

A:Cross-references: GB:M35669; NID:g197295; PIDN:AAA39004.1; PID:g309369

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 128;

Best Local Similarity 86.7%; Pred. No. 0.00011;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15

||||||| |||:|

Db 44 RASKSVSTSGYSYMH 58

RESULT 11

PN0446

Ig kappa chain precursor V-II region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0446

R:Kaluzza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimerization of monoclonal antibodies by inverse polym

A:Reference number: PN0444; MUID:93138402

A:Accession: PN0446

A:Molecule type: mRNA

A:Residues: 1-140 <KAL>

A:Cross-references: GB:L02345

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-140/Product: Ig light chain kappa-2 V region #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 140;

Best Local Similarity 86.7%; Pred. No. 0.00013;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15

||||||| |||:|

Db 44 RASKSVSTSGYSYMH 58

RESULT 12

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N:Alternate names: immunoglobulin light chain

C:Species: Mus musculus (house mouse)

C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68241; S68214

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

submitted to the EMBL Data Library, March 1994

A:Description: Specific peroxidase activity by formation of an antibody L-chain-porph

A:Reference number: S68241

A:Accession: S68241

A:Molecule type: mRNA

A:Residues: 1-218 <TAK>

A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

FEBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr

A:Reference number: S68211; MUID:96085223

A:Accession: S68214

A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: /NI', 3-212 <TAW>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 88.3%; Score 68; DB 2; Length 218;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNYMH 15
DB 24 RASKSVSASGYNYMH 38
|||||
|||||

RESULT 13
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase activity. It is directed against a porphyrin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 68; DB 2; Length 218;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNYMH 15
DB 24 RASKSVSASGYNYMH 38
|||||
|||||

RESULT 14
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Janot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioclonoma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 88.3%; Score 68; DB 2; Length 233;
Best Local Similarity 86.7%; Pred. No. 0.00021;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNYMH 15
DB 148 RASKSVSTSGYSYMH 162
|||||
|||||

RESULT 15
KWS40
Ig kappa chain V region (PC7940) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
C:Accession: C01938; A01938
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: C01938
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 85.7%; Score 66; DB 1; Length 111;
Best Local Similarity 86.7%; Pred. No. 0.00022;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASKSVSASGYNYMH 15
DB 24 RASKSVSASGYNYMH 38
|||||
|||||

Search completed: June 28, 2001, 15:58:46
Job time: 374 sec

Fri Jun 29 08:05:01 2001

us-09-724-406-28.rpr

Page 5

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:39 ; Search time 105.36 Seconds
(without alignments)
4.877 Million cell updates/sec

Title: US-09-724-406-28
Perfect score: 77
Sequence: 1 RASKSVASGYNM 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	88.3	111	1	KV3R_MOUSE
2	68	88.3	111	1	KV3S_MOUSE
3	68	88.3	111	1	KV3U_MOUSE
4	66	85.7	111	1	KV3T_MOUSE
5	64	83.1	108	1	KV3V_MOUSE
6	42	54.5	111	1	KV3H_MOUSE
7	42	54.5	111	1	KV3J_MOUSE
8	42	54.5	111	1	KV3K_MOUSE
9	42	54.5	131	1	KV3I_MOUSE
10	41	53.2	221	1	LEG6_TACTR
11	41	53.2	301	1	YGBI_HAEIN
12	41	53.2	608	1	XYNC_FIBSU
13	40	51.9	320	1	MEC3_CAEVU
14	40	51.9	321	1	MEC3_CAEEL
15	40	51.9	2468	1	MAPB_HUMAN
16	39	50.6	111	1	KV3C_MOUSE
17	38	49.4	132	1	KV3F_MOUSE
18	38	49.4	334	1	ARGC_BUCAL
19	38	49.4	816	1	NP22_MOUSE
20	37.5	48.7	421	1	P2X5_HUMAN
21	37	48.1	265	1	KNH1_CANGA
22	37	48.1	407	1	CHLP_SYNY3
23	36.5	47.4	374	1	PEL3_ERWCA
24	36.5	47.4	375	1	PEL3_ERWCH
25	36	46.8	111	1	KV3L_MOUSE
26	36	46.8	239	1	US21_HCMVA
27	36	46.8	253	1	YE24_MYCTO
28	36	46.8	437	1	SGCC_ECOLI
29	36	46.8	590	1	YM72_YEAST
30	35.5	46.1	1651	1	CO3_NAJNA
31	35	45.5	121	1	RL20_CHLPN
32	35	45.5	123	1	RL20_CHLTR
33	35	45.5	195	1	VM72_INBLE

34	35	45.5	295	1	MEC3_CAEBR	P34764	caenorhabdi
35	35	45.5	378	1	AGAL_COFAR	Q42656	coffea arab
36	35	45.5	419	1	CLPX_CHLTR	O84711	chlamydia t
37	35	45.5	445	1	6PGD_CITDI	P41582	citrobacter
38	35	45.5	445	1	6PGD_CITFR	P41583	citrobacter
39	35	45.5	445	1	6PGD_ESCVU	P41574	escherichia
40	35	45.5	445	1	6PGD_KLEPL	P41575	klebsiella
41	35	45.5	445	1	6PGD_KLETE	P41578	shigella bo
42	35	45.5	445	1	6PGD_SHIBO	P41579	shigella dy
43	35	45.5	445	1	6PGD_SHIDY	P41580	shigella so
44	35	45.5	445	1	6PGD_SHISO	P77915	pseudomonas
45	35	45.5	460	1	HEMN_PSEAE		

ALIGNMENTS

RESULT 1
KV3R_MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6684.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01938; KVM584;
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
BY SIMILARITY.

Query Match 88.3%; Score 68; DB 1; Length 111;
Best Local Similarity 86.7%; Pred No. 3e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKSVASGYNM 15
DB 24 RASKSVSTSGSYMH 38
||||| |||:|

RESULT 2
KV3S_MOUSE
ID KV3S_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 108
 FT DISULFID 23 92
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;

Query Match 83.1%; Score 64; DB 1; Length 108;
 Best Local Similarity 80.0%; Pred. No. 0.00015;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKSVSASGYNMH 15
 |||:|||||:|||||
 DB 24 RASQSVSTSGYSYMH 38

RESULT 6
 ID KV3H_MOUSE STANDARD; PRT; 111 AA.
 AC P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
 DR PIR; A01934; KWS37.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 54.5%; Score 42; DB 1; Length 111;
 Best Local Similarity 53.3%; Pred. No. 1.2;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 RASKSVSASGYNMH 15
 |||:|||||:|||||
 DB 24 RASESVDSYGNFSMH 38

RESULT 7
 ID KV3J_MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR; A01935; KWSM6.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region.

OY 1 RASKSVSASGYNMH 15
 |||:|||||:|||||
 DB 24 RASESVDSYGNFSMH 38

ID KV3J_MOUSE STANDARD; PRT; 111 AA.
 AC P01662;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (ABPC 22).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
 DR PIR; A01935; KWSM6.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 54.5%; Score 42; DB 1; Length 111;
 Best Local Similarity 53.3%; Pred. No. 1.2;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 RASKSVSASGYNMH 15
 |||:|||||:|||||
 DB 24 RASESVDSYGNFSMH 38

RESULT 8
 ID KV3K_MOUSE STANDARD; PRT; 111 AA.
 AC P01663;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 4050.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 diversity.";
 RL Nature 276:785-790(1978).
 DR PIR; A01935; KWSM6.
 DR InterPro: IPR003006; -.
 DR Pfam; PF00047; ig; 1.
 KW Immunoglobulin V region.

OY 1 RASKSVSASGYNMH 15
 |||:|||||:|||||
 DB 24 RASESVDSYGNFSMH 38

RESULT 7
 KV3J_MOUSE

FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 54.5%; Score 42; DB 1; Length 111;
 Best Local Similarity 53.3%; Pred. No. 1.2;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKSVASGYNYMH 15
 |||:|:|:|:|:
 Db 24 RASESVDSYGNFSMH 38

RESULT 9
 KV31_MOUSE STANDARD; PRT; 131 AA.
 AC P01661;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE OF 1-35.
 RX MEDLINE=78235887; PubMed=98179;
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 the variable and constant regions of immunoglobulin light chain
 precursors: implications on the organization and controlled
 expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]

RP SEQUENCE OF 21-131.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 kappa chains with limited sequence differences.";
 RL Biochemistry 12:760-771(1973).
 RN [3]

RP REVISIONS.
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR PIR: A01935; KVM5M6;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 54.5%; Score 42; DB 1; Length 131;
 Best Local Similarity 53.3%; Pred. No. 1.4;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKSVASGYNYMH 15
 |||:|:|:|:|:
 Db 44 RASESVDSYGNFSMH 58

RESULT 10
 LEC6_TACTR STANDARD; PRT; 221 AA.
 ID LEC6_TACTR
 AC P82151;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LECTIN L6.
 OS Tachyplesus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 OX NCBI_TaxID=6853;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Hemocyte;
 RX MEDLINE=95301536; PubMed=7782311;
 RA Saito T., Kawabate S.-I., Hirata M., Iwanaga S.;
 RT "A novel type of limulus lectin-L6. Purification, primary structure,
 and antibacterial activity.";
 RL J. Biol. Chem. 270:14493-14499(1995).
 CC -!- FUNCTION: LIPOPOLYSACCHARIDE-BINDING PROTEIN WITH GRAM-NEGATIVE
 ANTIBACTERIAL ACTIVITY. BINDS ZINC AND CALCIUM.

CC -!- SUBCELLULAR LOCATION: L-GRANULES.
 CC -!- TISSUE SPECIFICITY: HEMOCYTES.
 CC -!- SIMILARITY: BELONGS TO THE TECTONIN FAMILY.
 KW Lectin; Antibiotic; Zinc; Calcium; Metal-binding; Alkylation; Repeat.

FT DOMAIN 1 221 6 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 1 38 1.
 FT REPEAT 39 75 2.
 FT REPEAT 76 113 3.
 FT REPEAT 114 150 4.
 FT REPEAT 151 188 5.
 FT REPEAT 189 221 6.
 FT MOD_RES 201 201 ALKYLATION.

FT DISULFID 32 36
 FT DISULFID 108 112
 FT DISULFID 183 187
 SQ SEQUENCE 221 AA; 24410 MW; 59C97CF736DF4962 CRC64;

Query Match 53.2%; Score 41; DB 1; Length 221;
 Best Local Similarity 72.7%; Pred. No. 3.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KSVASGYNYM 14
 | | | | | | | |
 Db 86 KHVSASGYGYI 96

RESULT 11
 YGBJ_HAEIN STANDARD; PRT; 301 AA.
 ID YGBJ_HAEIN
 AC P44979;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL PROTEIN HI1010.
 GN HI1010.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]

SEQUENCE FROM N.A.
 RP STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).
 CC -1- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE
 CC FAMILY. STRONG, TO E.COLI YGBJ.
 CC -----
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 CC -----
 DR EMBL; U32782; AAC22671.1; -;
 DR TIGR; H11010; -;
 DR InterPro: IPR002204; -;
 DR PROSITE; PS00895; 3-HYDROXYISOBUT_DH; 1.
 KW Hypothetical protein; Oxidoreductase; NAD.
 FT ACT_SITE 177 177 BY SIMILARITY.
 SQ SEQUENCE 301 AA; 31035 MW; 7C615A25B0947D18 CRC64;

Query Match 53.2%; Score 41; DB 1; Length 301;
 Best Local Similarity 46.2%; Pred. No. 5.2;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SKSVASAGYNYMH 15
 :L:::|:::|
 DB 49 AKAVAANGYDFAH 61

RESULT 12
 XNFC_FIBSU STANDARD; PRT; 608 AA.
 ID XNFC_FIBSU STANDARD; PRT; 608 AA.
 AC P35811;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ENDO-1,4-BETA-XYLANASE C PRECURSOR (EC 3.2.1.8) (XYLANASE C)
 DE (1,4-BETA-D-XLAN XLANOHYDROLASE C).
 GN XNFC.
 OS Fibrobacter succinogenes (Bacteroides succinogenes).
 OC Bacteria; Fibrobacter/Acidobacteria group; Fibrobacter group;
 OC Fibrobacter.
 OX NCBI_TaxID=833;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-41.
 RC STRAIN=S85;
 RX MEDLINE=94064561; PubMed=8244936;
 RA Paradis F.W., Zhu H., Krell P.J., Phillips J.P., Forsberg C.W.;
 RT "The xnc gene from Fibrobacter succinogenes S85 codes for a xylanase
 RT with two similar catalytic domains.";
 RL J. Bacteriol. 175:7666-7672(1993).
 CC -1- FUNCTION: CELAVES XYLANS WITH THE PRODUCTION OF XULOSE, XYLOBIOS
 CC AND XYLO-OLIGOSACCHARIDES.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).

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 CC -----
 DR EMBL; U01037; AAA21848.1; -;
 DR HSSP; P36218; LXYN
 DR InterPro: IPR001137; -;
 DR Pfam; PF00457; Glyco_Hydro_11; 2.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HVDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HVDROL_F11_2; 1.
 KW Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
 KW Signal; Repeat.
 FT SIGNAL 1 25
 FT CHAIN 26 608 ENDO-1,4-BETA-XYLANASE C.
 FT DOMAIN 26 262 XYLANASE DOMAIN 1.
 FT DOMAIN 263 285 SER-RICH (LINKER).
 FT DOMAIN 286 529 XYLANASE DOMAIN 2.
 FT DOMAIN 530 543 SER-RICH (LINKER).
 FT ACT_SITE 142 142 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 237 237 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 409 409 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 501 501 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 608 AA; 66415 MW; 7FA338016F5857CE CRC64;

Query Match 53.2%; Score 41; DB 1; Length 608;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SKSVASAGYNYMH 14
 :L:::|:::|
 DB 386 SKOGSAGGYNYI 397

RESULT 13
 MEC3_CAEVU STANDARD; PRT; 320 AA.
 ID MEC3_CAEVU STANDARD; PRT; 320 AA.
 AC F34765;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE MECHANOSENSORY PROTEIN 3.
 GN MEC-3.
 OS Caenorhabditis vulgaris.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=31233;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084094; PubMed=1684166;
 RA Way J.C., Wang L., Run J.Q., Wang A.;
 RT "The mec-3 gene contains cis-acting elements mediating positive and
 RT negative regulation in cells produced by asymmetric cell division in
 RT Caenorhabditis elegans.";
 RL Genes Dev. 5:2193-2211(1991).
 CC -1- FUNCTION: MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH
 CC RECEPTOR NEURONS. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86
 CC TO SITES IN THE MEC-3 GENE PROMOTER.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.

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 CC -----

DR EMBL: X63956; CAA45377.1; -
 DR PIR: A39479; A39479.
 DR HSP: P06601; IFJL.
 DR TRANSFAC: T01970; -
 DR InterPro: IPR001356; -
 DR InterPro: IPR001781; -
 DR Pfam: PF00412; LIM; 2.
 DR Pfam: PF00046; homeobox; 1.
 DR PROSITE: PS00027; HOMEBOX_1; FALSE_NEG.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS00023; LIM_DOMAIN_2; 2.
 DR Homeobox; DNA-binding; Nuclear protein; Developmental protein;
 KW Repeat; LIM motif; Metal-binding; Zinc.
 KW DOMAIN 29 79 LIM.
 FT DOMAIN 89 145 HOMEBOX.
 FT DNA_BIND 216 275
 FT DOMAIN 314 320 ASP/GLU-RICH (ACIDIC).
 SQ SEQUENCE 320 AA; 36849 MW; AF98BD31C2B2FDB6 CRC64;

Query Match 51.9%; Score 40; DB 1; Length 320;
 Best Local Similarity 46.7%; Pred. No. 8.3;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RASKSVSASGYNYMH 15
 : | | | | | | | |
 Db 186 QVKKEVDAYGINFEH 200

RESULT 14
 ID MEC3_CAEEL STANDARD; PRT; 321 AA.
 AC P09088;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE MECHANOSENSORY PROTEIN 3.
 GN MEC-3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88253425; PubMed=2898300;
 RA Way J.C., Chalfie M.;
 RT "mec-3, a homeobox-containing gene that specifies differentiation of
 RT the touch receptor neurons in *C. elegans*.";
 RL Cell 54:5-16(1988).
 RN [2]
 RP REVISIONS. SEQUENCE FROM N.A.
 RX MEDLINE=93099872; PubMed=1361171;
 RA Xue D., Finney M., Ruvkun G., Chalfie M.;
 RT "Regulation of the mec-3 gene by the *C.elegans* homeoproteins UNC-86
 RT and MEC-3.";
 RL EMBO J. 11:4969-4979(1992).
 CC -1- FUNCTION: MEC-3 SPECIFIES DIFFERENTIATION OF THE SET OF SIX TOUCH
 CC RECEPTOR NEURONS. BINDS COOPERATIVELY AS A HETERODIMER WITH UNC-86
 CC TO SITES IN THE MEC-3 GENE PROMOTER.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: TO OTHER HOMEBOX DOMAINS. BELONGS TO THE LIM
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -----

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DR EMBL: L02877; AAA50514.1; -
 DR EMBL: M20244; AAA28108.1; ALT_SEQ.
 DR PIR: A27662; A27662.
 DR PIR: S28390; S28390.
 DR HSP: P06601; IFJL.
 DR TRANSFAC: T01076; -
 DR InterPro: IPR001356; -
 DR InterPro: IPR001781; -
 DR Pfam: PF00412; LIM; 2.
 DR Pfam: PF00046; homeobox; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS00023; LIM_DOMAIN_2; 2.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Nuclear protein; Developmental protein;
 KW Repeat; LIM motif; Metal-binding; Zinc.
 KW DOMAIN 29 79 LIM.
 FT DOMAIN 89 145 HOMEBOX.
 FT DNA_BIND 217 276 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 315 321
 SQ SEQUENCE 321 AA; 37088 MW; 9231E7C3F5054853 CRC64;

Query Match 51.9%; Score 40; DB 1; Length 321;
 Best Local Similarity 46.7%; Pred. No. 8.3;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RASKSVSASGYNYMH 15
 : | | | | | | | |
 Db 187 QVKKEVDAYGINFEH 201

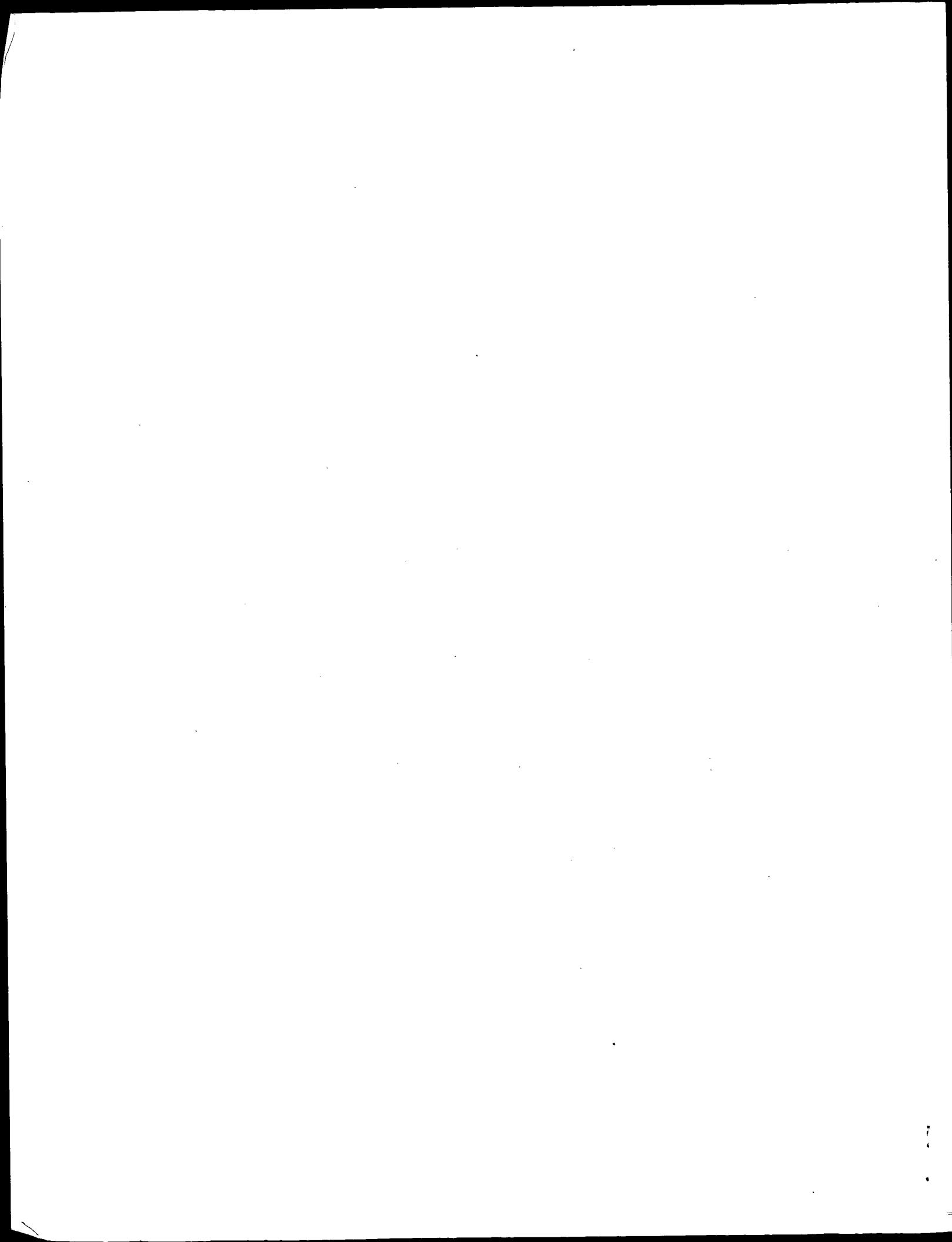
RESULT 15
 ID MAPB_HUMAN STANDARD; PRT; 2468 AA.
 AC P46821;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: MAP1 LIGHT CHAIN LC1].
 GN MAP1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104835; PubMed=7806212;
 RA Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
 RT "Cloning of human microtubule-associated protein 1B and the
 RT identification of a related gene on chromosome 15.";
 RL Genomics 22:273-280(1994).
 CC -1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
 CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
 CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
 CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
 CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
 CC STABILIZING MICROTUBULES.
 CC -1- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
 CC WITH MAP1A AND MAP1B PROTEINS.
 CC -1- DOMAIN: HAS A HIGHLY BASIC REGION WITH MANY COPIES OF THE SEQUENCE
 CC KKEE AND KKEIV/, REPEATED BUT NOT AT FIXED INTERVALS. THIS LATTER
 CC BOTH IN VITRO AND IN VIVO.
 CC -1- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED
 CC FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
 CC BOTH MAP1A AND MAP1B.

CC -!- SIMILARITY: TO NEURAXIN.
 CC -----
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 CC -----

DR EMBL: L06237; AAA18904.1; -
 DR MIM: 157129; -
 DR InterPro: IPR000102; -
 DR Pfam: PF00414; MAP1B_neuraxin: 10.
 DR PROSITE: PS00230; MAP1B_NEURAXIN: 6.
 KW Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 FT 12 X 17 AA TANDEM REPEATS.
 FT DOMAIN 1869 2074
 FT REPEAT 1869 1885 1.
 FT REPEAT 1886 1902 2.
 FT REPEAT 1903 1919 3.
 FT REPEAT 1920 1936 4.
 FT REPEAT 1937 1953 5.
 FT REPEAT 1954 1970 6.
 FT REPEAT 1971 1987 7.
 FT REPEAT 1988 2004 8.
 FT REPEAT 2005 2021 9.
 FT REPEAT 2022 2038 10.
 FT REPEAT 2039 2055 11.
 FT REPEAT 2056 2072 12.
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 51.9%; Score 40; DB 1; Length 2468;
 Best Local Similarity 61.5%; Pred. No. 70;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RASKSVSASGNY 13
 | : | | | | |
 Db 1911 RTTKSPFSDGYSY 1923

Search completed: June 28, 2001, 15:54:39
 Job time: 127 sec



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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:26 ; Search time 411.58 Seconds
(without alignments)
4.822 Million cell updates/sec

Title: US-09-724-406-28

Perfect score: 77

Sequence: 1 RASKSVASAGNYMH 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.unclassified:*
- 13: sp.vertebrate:*
- 14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	44	57.1	477	10	Q9ZWP7
2	43	55.8	90	2	Q9L817
3	43	55.8	240	2	Q47197
4	43	55.8	240	2	O30925
5	42	54.5	764	10	Q9L275
6	41	53.2	114	3	P78570
7	41	53.2	203	5	Q9U5E9
8	41	53.2	232	5	Q9NXX8
9	41	53.2	233	10	O65278
10	41	53.2	256	5	Q9NB63
11	41	53.2	377	10	Q9FWU1
12	41	53.2	2693	13	Q9L908
13	41	53.2	3469	5	Q9U412
14	41	53.2	3502	5	Q9VYJ9
15	40	51.9	328	5	O02240
16	40	51.9	492	5	O76263
17	40	51.9	662	2	Q9RXR4
18	40	51.9	1049	5	Q9VSV5
19	40	51.9	1095	5	Q9TVG7

20	39.5	51.3	257	2	Q9KJT6	Q9kjt6 staphylococ
21	39	50.6	112	14	Q82092	Q82092 human rhino
22	39	50.6	170	11	Q9QYL0	Q9qyl0 mus musculo
23	39	50.6	445	2	Q59473	Q59473 k 6-phospho
24	39	50.6	1122	13	P70047	P70047 xenopus lae
25	39	50.6	1518	5	Q9VN58	Q9vn58 drosophila
26	38	49.4	60	5	Q9NE91	Q9ne91 leishmania
27	38	49.4	150	10	Q9M4Y8	Q9m4y8 cucumis sat
28	38	49.4	229	2	Q9KYG2	Q9kyg2 streptomyce
29	38	49.4	241	2	Q9KSQ5	Q9ksq5 vibrio chol
30	38	49.4	254	3	Q9P734	Q9p734 neurospora
31	38	49.4	284	2	Q9WXL1	Q9wxe1 rhodovulum
32	38	49.4	288	10	Q96256	Q96256 arabidopsis
33	38	49.4	292	6	Q9XT99	Q9xt99 oryctolagus
34	38	49.4	317	10	O48720	O48720 arabidopsis
35	38	49.4	377	10	Q9M1P0	Q9m1p0 arabidopsis
36	38	49.4	415	10	Q9SJH8	Q9sjh8 arabidopsis
37	38	49.4	469	5	Q9VF93	Q9vf93 drosophila
38	38	49.4	494	5	Q9NIN7	Q9nin7 drosophila
39	37.5	48.7	263	2	O54487	O54487 staphylococ
40	37.5	48.7	353	2	Q04086	Q04086 erwinia car
41	37	48.1	56	2	Q9X678	Q9x678 prevotella
42	37	48.1	113	10	O42025	O42025 arabidopsis
43	37	48.1	181	9	Q37970	Q37970 bacterioph
44	37	48.1	245	2	Q9WJ6	Q9wj6 blastomonas
45	37	48.1	253	2	O32402	O32402 rhodocyclu

ALIGNMENTS

RESULT 1

Q9ZWP7 ID Q9ZWP7 PRELIMINARY: PRT: 477 AA.
AC Q9ZWP7;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE RNA-DEPENDENT RNA POLYMERASE.
OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; rosids I;
OC Rosales; Rosaceae; Pyrus.
OX NCBI_TaxID=3767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99138178; PubMed=9972231;
RA Osaki H., Kudo A., Ohtsu Y.;
RT "Nucleotide sequence of seed- and pollen-transmitted double-stranded
RT RNA, which encodes a putative RNA polymerase, detected
RT from Japanese pear."
RL Biosci. Biotechnol. Biochem. 62:2101-2106(1998).
DR EMBL; AB013616; BAA34783.1; -;
KW RNA-directed RNA polymerase.
SQ SEQUENCE 477 AA; 54908 MW; 071E9797E6B1C2F2 CRC64;

Query Match 57.1%; Score 44; DB 10; Length 477;

Best Local Similarity 72.7%; Pred. No. 8.4;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KSVASAGNYM 14

DB 125 KSSTAAGNYM 135

RESULT 2

Q9L817 ID Q9L817 PRELIMINARY: PRT: 90 AA.
AC Q9L817;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

Best Local Similarity 50.0%; Pred. No. 33;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 ASKVSASGYNM 15
DB 13 SOKNVAASGHNHH 26

RESULT 6
P78570 ID P78570 PRELIMINARY; PRT; 114 AA.
AC P78570;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE I (EC 2.7.7.6) (RNA POLYMERASE II) (RNA
DE POLYMERASE III) (RNA NUCLEOTIDYLTRANSFERASE (DNA-DIRECTED))
DE (FRAGMENT).
GN RPAB.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
OC Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HORST U1;
RX MEDLINE=97111990; PubMed=8953726;
RA Sonnenberg A.S.M., De Groot P.W.J., Schaap P.J., Baars J.J.P.,
R Visser J., van Griensven L.J.L.D.;
RT "Isolation of expressed sequence tags of Agaricus bisporus and their
RT assignment to chromosomes.";
RL Appl. Environ. Microbiol. 62:4542-4547(1996).
CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE +
CC RNA(N) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
DR EMBL; X94765; CAA64391.1; -;
DR InterPro; IPR001572; -;
DR Pfam; PF00552; RNA_pol_B; 1.
KW DNA-directed RNA polymerase; Nucleotidyltransferase; Transcription;
KW Transferase.
FT NON_TER 1 1
FT 114 114
SQ SEQUENCE 114 AA; 12903 MW; 656C52B0AE6C2908 CRC64;

Query Match 53.2%; Score 41; DB 3; Length 114;
Best Local Similarity 70.0%; Pred. No. 6.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KVSASGYN 13
DB 20 KLSAAGYN 29
RESULT 7
Q9U5E9 ID Q9U5E9 PRELIMINARY; PRT; 203 AA.
AC Q9U5E9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TACHYLECTIN-P (FRAGMENT).
GN TL-P.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20076430; PubMed=10608824;
RA Nagai T., Kawabata, S., Shishikura F., Sugita H.;
RT "Purification, characterization, and amino acid sequence of an
RT embryonic lectin in perivitelline fluid of the horseshoe crab.";

J. Biol. Chem. 274:37673-37678(1999).
DR EMBL; AB028144; BAA88574.1; -;
FT NON_TER 1 1
FT NON_TER 203 203
SQ SEQUENCE 203 AA; 22550 MW; 30900733AC2C89D2 CRC64;

Query Match 53.2%; Score 41; DB 5; Length 203;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KVSASGYNM 14
DB 85 KHSASGYGI 95
RESULT 8
Q9NKX8 ID Q9NKX8 PRELIMINARY; PRT; 232 AA.
AC Q9NKX8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TACHYLECTIN-1 EMBRYO (FRAGMENT).
GN TL-LEMB
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE BODY;
RA Nagai T., Kawabata S., Sugita H.;
RT "Tachylectin-1emb.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037394; BAA90326.1; -;
FT NON_TER 1 1
SQ SEQUENCE 232 AA; 25820 MW; CBD4BFF289F852D1 CRC64;

Query Match 53.2%; Score 41; DB 5; Length 232;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KVSASGYNM 14
DB 85 KHSASGYGI 95
RESULT 9
O65278 ID O65278 PRELIMINARY; PRT; 233 AA.
AC O65278;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE F6N23.7 PROTEIN.
GN F6N23.7 OR AT4G00690.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WASHU;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Geisel C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Waterston R.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
[4]
RA SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RA SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF058919; AAC13629.1; -;
DR EMBL: AL161472; CAB80878.1; -;
DR MEROPS; C48.001; -;
DR Mendel; 28980; Arabidopsis; 28980.
DR InterPro; IPR003653; -;
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 27632 MW; 46A1E31F70EC86B8 CRC64;

Query Match 53.2%; Score 41; DB 10; Length 233;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 KVSASGNY 13
| | | | |
Db 85 KLVSGSY 94

RESULT 10
Q9NB63 PRELIMINARY; PRT; 256 AA.
AC Q9NB63;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE GALACTOSE-BINDING PROTEIN
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
[1]
RA SEQUENCE FROM N.A.
RA Chen S.-C., Yeh M.-S., Chiou S.-T., Huang C.-J., Liu T.-Y.;
RT "Genomic structure of galactose-binding protein from the hemolymph of
RT Taiwanese horseshoe crab."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF264067; AAF74773.1; -;
SQ SEQUENCE 256 AA; 28517 MW; 5EC0272B88F44FF8 CRC64;

Query Match 53.2%; Score 41; DB 5; Length 256;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 KVSASGNY 14
| | | | |
Db 109 KVSASGY 119

RESULT 11
Q9FWU1 PRELIMINARY; PRT; 377 AA.
AC Q9FWU1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 39.3 KDA PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae;
OC Oryza.
OX NCBI_TaxID=4530;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBa0051D19 genomic sequence."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC023240; AAG13534.1; -;
KW Hypothetical protein.
SQ SEQUENCE 377 AA; 39255 MW; 28E1C75270877C4D CRC64;

Query Match 53.2%; Score 41; DB 10; Length 377;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 ASKVSASGNY 15
| | | | |
Db 227 AAASCHASGY 240

RESULT 12
Q91908 PRELIMINARY; PRT; 2693 AA.
ID Q91908;
AC Q91908;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INOSITOL 1,4,5-TRIPHOSPHATE RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=93258819; PubMed=8387895;
RA Kume S., Muto A., Aruga J., Nakagawa T., Michikawa T., Furuichi T.,
RA Nakade S., Okano H., Mikoshiba K.;
RT "The Xenopus IP3 receptor: structure, function, and localization in
RT oocytes and eggs."
RL Cell 73:555-570(1993).
DR EMBL: D14400; BAA03304.1; -;
DR InterPro; IPR000493; -;
DR InterPro; IPR000699; -;
DR InterPro; IPR001682; -;
DR InterPro; IPR003608; -;
DR Pfam; PF01365; RYDR.1TBR.1.
DR PRINTS; PR00779; INSP3RECEPTR.
DR SMART; SM00472; MIR; 1.
KW Calcium channel.
SQ SEQUENCE 2693 AA; 306670 MW; CBF6AF6FEF16A753C CRC64;

Query Match 53.2%; Score 41; DB 13; Length 2693;
Best Local Similarity 61.5%; Pred. No. 2e+02; 4; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 1;
QY 1 RASKVSASGNY 13
| | | | |
Db 1139 KAKKSESTSSNY 1151

RESULT 13
Q9U412 PRELIMINARY; PRT; 3469 AA.
ID Q9U412
AC Q9U412;

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE SANT DOMAIN PROTEIN SMTER.
 GN SMR OR SMTER OR CG4013.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=99417957; PubMed=10488333;
 RA Tsai C.-C., Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.;
 RT "SMTER, a Drosophila nuclear receptor coregulator, reveals that Ecr-
 mediated repression is critical for development.";
 RL MOL. Cell 4:175-186(1999).
 DR EMBL; AF175223; AAD52614.1; -.
 DR FlyBase; FBgn0024308; Smr.
 DR InterPro; IPR000104; -.
 DR InterPro; IPR001005; -.
 DR InterPro; IPR002086; -.
 DR Pfam; PF00249; myb_DNA-binding; 1.
 DR PRINTS; PR00308; ANTIFREEZE1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
 DR SMART; SM00395; SANT; 1.
 SQ SEQUENCE 3469 AA; 364115 MW; 6284E14C5C247CD9 CRC64;

 Query Match 53.2%; Score 41; DB 5; Length 3469;
 Best Local Similarity 63.6%; Pred. No. 2.6e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 ASKVSASGYN 12
 Db 1208 ASKAINAEGYN 1218
 |||:::| |||

 RESULT 14
 Q9VYJ9 PRELIMINARY; PRT; 3502 AA.
 ID Q9VYJ9
 AC Q9VYJ9
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE SMR PROTEIN.
 GN SMR OR CG4013.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731133;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei H., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; -.
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003490; AAF48196.1; -.
 DR FlyBase; FBgn0024308; Smr.
 DR InterPro; IPR000104; -.
 DR InterPro; IPR001005; -.
 DR InterPro; IPR002086; -.
 DR Pfam; PF00249; myb_DNA-binding; 1.
 DR PRINTS; PR00308; ANTIFREEZE1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 DR SMART; SM00395; SANT; 1.
 SQ SEQUENCE 3502 AA; 369068 MW; 74C8004F9DA8F8D9 CRC64;

 Query Match 53.2%; Score 41; DB 5; Length 3502;
 Best Local Similarity 63.6%; Pred. No. 2.7e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 ASKVSASGYN 12
 Db 1347 ASKAINAEGYN 1357
 |||:::| |||

 RESULT 15
 Q02240 PRELIMINARY; PRT; 328 AA.
 ID Q02240
 AC Q02240
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE MEC-3 PROTEIN.
 GN MEC-3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RX SEQUENCE FROM N.A.
 RA Wild A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RX [2]
 RX MEDLINE=99006961; PubMed=9851916;
 none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS LIM DOMAIN(S). THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -1- SIMILARITY: TO OTHER HOMEBOX DOMAINS.
 DR EMBL; Z81054; C2B02885.2; -.
 DR HSSP; P14859; IFOG.
 DR InterPro; IPR000047; -.

DR InterPro; IPR001356; -.
 DR InterPro; IPR001781; -.
 DR Pfam; PF00046; homeobox; 2.
 DR Pfam; PF00412; LIM; 4.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR PRODOM; PD000094; -; 2.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS0071; HOMEBOX_2; 1.
 DR PROSITE; PS00478; LIM_DOMAIN_1; UNKNOWN_1.
 DR PROSITE; PS0023; LIM_DOMAIN_2; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 1.
 KW DNA-binding; Homeobox; LIM motif; Metal-binding; Nuclear protein;
 KW Zinc.
 SQ SEQUENCE 328 AA; 37953 MW; 3287768804CDC253 CRC64;

Query Match 51.9%; Score 40; DB 5; Length 328;
 Best Local Similarity 46.7%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RASKSVSASGYNYMH 15
 : | | | | | :
 Db 194 QVKKEYDAYGYNFEH 208

Search completed: June 28, 2001, 16:08:27
 Job time: 955 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:38 ; Search time 362.28 Seconds
(without alignments)
1.171 Million cell updates/sec

Title: US-09-724-406-30
Sequence: 1 LASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	31	100.0	7 18 AAW27345	CDR2 from murine a
2	31	100.0	7 21 AAB09999	H. pylori HSP60-b1
3	31	100.0	7 16 AAR85179	GM-CSF receptor al
4	31	100.0	103 15 AAR47933	Light chain region
5	31	100.0	103 20 AAW89349	Mouse 23f2G light
6	31	100.0	107 18 AAW27353	Light chain variab
7	31	100.0	108 20 AAY13949	VL chain of anti-C
8	31	100.0	110 15 AAR60810	Light chain variab
9	31	100.0	111 15 AAR53930	Light chain variab
10	31	100.0	111 15 AAR60528	Light chain variab
11	31	100.0	111 17 AAR85242	Humanised antibody

12	31	100.0	111	17	AAR85236	Murine 206 antibod
13	31	100.0	111	20	AAW89351	Humanised 23f2G l1
14	31	100.0	111	21	AAB10019	H. pylori HSP60-b1
15	31	100.0	112	12	AAR10539	Chimeric MAB 9.2.2
16	31	100.0	112	16	AAR79158	Human IgE receptor
17	31	100.0	112	16	AAR80272	VI region from an
18	31	100.0	112	16	AAR79156	Human IgE receptor
19	31	100.0	112	18	AAW27358	Light chain variab
20	31	100.0	112	18	AAW27527	Light chain variab
21	31	100.0	131	13	AAR28668	p12-k2. Synthetic
22	31	100.0	237	20	AAW73873	Human antiFc epsil
23	31	100.0	240	20	AAW73875	Human antiFc epsil
24	31	100.0	260	16	AAR77617	Anti-C5 MAB N19/8
25	31	100.0	3096	22	AAW46770	FANCIP3 protein fr
26	29	93.5	215	15	AAR74781	Light chain of 59.
27	29	93.5	230	11	AAR06610	Intact natural cut
28	29	93.5	230	15	AAR46295	F. solani pisi pre
29	29	93.5	230	15	AAR59796	Fusarium solani pi
30	29	93.5	230	15	AAR59801	Fusarium solani pi
31	28	90.3	87	16	AAR80081	Mouse derived ligh
32	28	90.3	91	20	AAW95478	Mouse derived RT3
33	28	90.3	110	15	AAR60564	Anti-carcinoembryo
34	28	90.3	110	20	AAW39532	Murine COL1 VK cha
35	28	90.3	110	20	AAW39534	Humanised Murine C
36	28	90.3	110	20	AAW39535	Humanised Murine C
37	28	90.3	110	20	AAW39544	Humanised Murine C
38	28	90.3	110	20	AAW39546	Humanised Murine C
39	28	90.3	111	15	AAR48622	Sequence of the hu
40	28	90.3	111	15	AAR48623	Sequence of the hu
41	28	90.3	111	15	AAR65172	Murine NM-01 varia
42	28	90.3	111	16	AAR65174	Region producing h
43	28	90.3	121	14	AAR33346	Sequence of the va
44	28	90.3	121	15	AAR48615	Sequence of the mo
45	28	90.3	121	17	AAW09259	Monoclonal antibod

ALIGNMENTS

RESULT 1
AAW27345
ID AAW27345 standard; peptide; 7 AA.
XX
AC AAW27345;
XX
DT 12-DEC-1997 (first entry)
XX
DE CDR2 from murine anti-human IgE receptor antibody heavy chain.
XX
KW Complementarity determining region; CDR2; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAB; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy.
XX
OS Mus spp.
XX
PN JP09191886-A.
XX
PD 29-JUL-1997.
XX
PF 19-JAN-1996; 96JP-0024816.
XX
PR 19-JAN-1996; 96JP-0024816.
XX
PA (ASAK) ASAKI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKY KK.
PA (TORI) TORII YAKUHN KK.
PA (TSUR/) TSURA T.
XX
DR WPI; 1997-429186/40.
XX
PT Humanised, semi-chimeric and chimeric antibodies against human
high-affinity IgE receptor - useful medicinally and have low

PT antigenicity in humans
 PS Claim 1; Page 12; 26pp: Japanese.
 XX
 CC The present complementarity determining region 2 (CDR2), which is
 CC from a murine, anti-human high affinity immunoglobulin E (IgE)
 CC receptor, monoclonal antibody (MAB) heavy chain variable region,
 CC can be used in the preparation of humanised or semi-chimeric
 CC anti-human high affinity IgE receptor MAB. The MAB can be used to
 CC treat or prevent diseases, specifically allergies, associated with
 CC the receptor. The humanised, semi-chimeric or chimeric MAB have
 CC very low antigenicity in humans.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 1 lasnles 7

RESULT 2
 AAB09999
 ID AAB09999 standard; Protein; 7 AA.
 XX
 AC AAB09999;
 XX
 DT 01-NOV-2000 (first entry)
 DE H. pylori HSP60-binding antibody light chain CDR2 protein fragment.
 XX
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heat shock protein; HSP60; light chain; CDR;
 KW complementarity determining region.
 XX
 OS Unidentified.
 XX
 PN WO200026671-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-EP08212.
 XX
 PR 29-OCT-1998; 98EP-0120517.
 PR 06-NOV-1998; 98EP-0120687.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringels A;
 XX
 DR WPI; 2000-365747/31.
 DR N-PSDB; AAA40155.
 XX
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage
 XX
 PS Claim 20; Page 20; 84pp: German.
 XX
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (MAB) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure;
 CC or (ii) a structure against which an antibody is produced by an animal

CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori heat shock protein,
 CC HSP60-binding antibody light chain complementarity determining region
 CC CDR1 which is used to illustrate the method of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 1 lasnles 7

RESULT 3
 AAR85179
 ID AAR85179 standard; peptide; 17 AA.
 XX
 AC AAR85179;
 XX
 DT 06-JUN-1996 (first entry)
 DE GM-CSF receptor alpha-chain binding peptide.
 XX
 KW Alpha-chain; GM-CSF; receptor; granulocyte; macrophage;
 KW colony stimulating factor; binding assay; antagonist;
 KW inflammation; autoimmune disease; agonist; upregulator;
 KW immune system cell; CDR II; light chain; antibody 23.2.
 XX
 OS Synthetic.
 XX
 PN WO9529690-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 26-APR-1995; 95WO-US05160.
 XX
 PR 29-APR-1994; 94US-0235404.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (WIST-) WISTAR INST.
 XX
 PI Kieber-Emmons T, Von Feldt JM, Weiner DB, Williams WV;
 PI
 XX WPI; 1995-392919/50.
 DR
 XX
 PT Identifying biologically active protein peptide mimics - by prepn.
 PT of recombinant antibody libraries and synthesising complementary
 PT determining region sequences.
 XX
 PS Example 2; Page 49; 70pp: English.
 XX
 CC The present peptide binds the alpha-chain of the GM-CSF receptor,
 CC and can therefore be used in binding assays in place of GM-CSF. It
 CC can also be used as an antagonist, i.e. in the treatment of
 CC inflammation or autoimmune diseases, or in the prodn. of GM-CSF
 CC agonists, i.e. upregulators for the prodn. of immune system cells.
 CC The peptide is derived from CDR II of the recombinant antibody
 CC light chain analogue of GM-CSF, 23.2.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 31; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 Db 2 lasnles 8

RESULT 4

AAW47933
 ID AAR47933 standard; Protein; 103 AA.

AC AAR47933;
 XX
 DT 24-JUL-1994 (first entry)
 XX
 DE Light chain region of 23F2G.
 XX
 KW Amplification: 23F2G; humanised antibody; heavy chain; light chain;
 KW hybridoma; inflammation; CD18; human leukocyte integrins; mAb 60.3;
 KW monoclonal antibody; LFA-1; adhesion; migration; multiple
 KW sclerosis; MS.

XX WO9402175-A.

XX
 XX
 PD 03-FEB-1994.

XX
 XX
 PF 16-JUL-1993; 93WO-US06734.

XX
 XX
 PR 16-JUL-1992; 92US-0915068.

XX
 XX
 PR 10-MAY-1993; 93US-0060699.

XX
 XX
 PA (ICOS-) ICOS CORP.

PA (UNIW) UNIV WASHINGTON.

XX
 XX
 PI Rose LM;

XX
 XX
 DR WPI: 1994-048551/06.

XX
 XX
 DR N-PSDB; AAQ35915.

XX Antibodies immunologically reactive with the CD18 of human
 PT leukocyte integrins and/or competing with mAb 60.3 for binding to
 PT human LFA-1 - for alleviating symptoms associated with
 PT inflammatory disease states
 XX
 PS Example 6; Page 43; 58pp; English.

XX Total RNA was isolated from the hybridoma cell line 23F2G and first
 CC strand cDNA was synthesised using the total RNA as a template. The
 CC first strand cDNA was used as a template for PCR to obtain double
 CC stranded DNA fragments encoding the variable regions of both the
 CC heavy and light chains of monoclonal antibody 23F2G. The sequence
 CC shown is that of the light chain variable region of MAb 23F2G
 CC The humanised form of MAb 23F2G may be administered to
 CC alleviate symptoms associated with inflammatory disease states, esp.
 CC for the inhibition of inflammatory processes associated with
 CC multiple sclerosis. The MAb blocks leukocyte adhesion and
 CC migration to inflammatory sites. The MAb is an anti-CD18 integrin
 CC antibody which competes with MAb 60.3 for binding to LFA-1.
 CC See also AAR47931-6.

XX Sequence 103 AA;

Query Match 100.0%; Score 31; DB 15; Length 103;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 Db 46 lasnles 52

RESULT 5

AAW89349
 ID AAW89349 standard; Protein; 103 AA.

XX
 AC AAW89349;

XX
 DT 02-MAR-1999 (first entry)

XX
 DE Mouse 23F2G light chain variable region.

XX
 KW Mouse; humanised; antibody; heavy chain variable region; light chain;
 KW 23F2G; inflammatory disease; multiple sclerosis; common beta chain;
 KW CD18; human leukocyte integrin.

XX
 OS Mus sp.

XX
 PN US5854070-A.

XX
 PD 29-DEC-1998.

XX
 PF 21-JAN-1997; 97US-0785571.

XX
 PR 16-JUL-1993; 93US-0094535.

XX
 PR 16-JUL-1992; 92US-0915068.

XX
 PR 10-MAY-1993; 93US-0060699.

XX
 PR 28-FEB-1995; 95US-0396089.

XX
 PR 21-JAN-1997; 97US-0785571.

XX
 PA (ICOS-) ICOS CORP.

PA (UNIW) UNIV WASHINGTON.

XX
 XX
 PI Rose LM;

XX
 XX
 DR WPI: 1999-094920/08.

XX
 DR N-PSDB; AAV81907.

XX
 PT Hydrindomas that secrete anti-CD18 antibody - useful for treating
 PT inflammation specifically multiple sclerosis

XX
 PS Example 6; Column 25-26; 24pp; English.

XX
 CC The present invention describes the hybridoma cell line 23F2G
 CC (ATCC HB 11801) and the Chinese hamster ovary (CHO) cell lines 6E6
 CC (ATCC CRL 11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAB)
 CC 23F2G (and its humanised variants 6E6 and B13-24) is an anti-human CD18
 CC antibody for the treatment of inflammation, specifically multiple
 CC sclerosis. The present sequence is mouse 23F2G light chain variable
 CC region from the present invention.

XX
 SQ Sequence 103 AA;

Query Match 100.0%; Score 31; DB 20; Length 103;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 Db 46 lasnles 52

XX
 DE Light chain variable region of human CRA2 antibody.

RESULT 6

AAW27353
 ID AAW27353 standard; Protein; 107 AA.

XX
 AC AAW27353;

XX
 DT 12-DEC-1997 (first entry)

XX
 DE Light chain variable region of human CRA2 antibody.

KW Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; light chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX Homo sapiens.

OS JP09191886-A.

PN 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASahi BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

DR N-PSDB; AAT90024.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medicinally and have low

PT antigenicity in humans

XX Disclosure; Fig 1; 26pp; Japanese.

XX The CDNA encoding the present sequence, the light chain variable
 CC region of the human antibody (Ab) CRA2, was used in the preparation
 CC of a humanised or semi-chimeric monoclonal Ab (MAB), comprising
 CC complementarity determining regions (CDR) from a murine, anti-human
 CC high affinity immunoglobulin E (IgE) receptor, MAB. The humanised,
 CC semi-chimeric or chimeric MAB can be used to treat or prevent
 CC diseases, specifically allergies, associated with the receptor, and
 CC has very low antigenicity in humans.

XX Sequence 107 AA;

Query Match 100.0%; Score 31; DB 18; Length 107;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LASNLES 7

Db 49 lasnles 55

RESULT 7

AA13949

ID AAY13949 standard; Protein; 108 AA.

XX AAY13949;

XX 14-JUL-1999 (first entry)

XX VL chain of anti-CD40 monoclonal antibody.

XX Inducer; antibody production; antigen-specific antibody; vaccine; HIV;
 KW B-cell activating signal; infectious disease; therapy; diagnosis.

XX Synthetic.

XX WO9922008-A1.

PN 06-MAY-1999.

XX 09-OCT-1998; 98WO-JP04563.

XX 27-OCT-1997; 97JP-0294393.

XX

PA (SUME) SUMITOMO ELECTRIC IND CO.

XX Sakaguchi N;

XX WPI; 1999-303020/25.

XX Inducer for production of antigen-specific antibody of high avidity

XX Example; Page 29-30; 36pp; Japanese.

XX This sequence is the VL chain of an anti-CD40 monoclonal antibody used in
 CC the construction of an inducer of the invention.

CC The inducer is for the production of an antigen-specific antibody with
 CC high avidity, consists of a chimeric molecule containing the antigen
 CC together with a B-cell activating signal. The inducer is a chimeric
 CC molecule containing: (1) an antigen portion recognised by a B-cell
 CC antigen receptor; and (2) a signal transmitter portion, such as anti-CD40
 CC antibody or its active fragments, which activates B-cells to produce the
 CC antigen-specific antibody. The inducer may be incorporated into a vaccine
 CC for prevention and treatment of infectious diseases including HIV, and
 CC used to produce antigen-specific monoclonal antibodies for the treatment,
 CC diagnosis and investigation of diseases.

XX Sequence 108 AA;

Query Match 100.0%; Score 31; DB 20; Length 108;

Best Local Similarity 100.0%; Pred. No. 8.2; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0;

OY 1 LASNLES 7

Db 50 lasnles 56

RESULT 8

AA60810

ID AAR60810 standard; Protein; 110 AA.

XX AAR60810;

XX 06-DEC-1994 (first entry)

XX Light chain variable region of antibody HCMV16.

XX Antibody; humanised antibody; variable region; immune response;
 KW cytomegalovirus; glycoprotein; complementarity determining region;
 KW CDR; heavy chain; light chain; ds.

XX Mus musculus.

XX WO9409136-A.

XX 28-APR-1994.

XX 15-OCT-1993; 93WO-GB02134.

XX 15-OCT-1992; 92GB-0021654.

XX (KETT-) KETTOCK LODGE CAMPUS 2.

XX Carr FU, Hamilton AA, Harris WJ;

XX WPI; 1994-151321/18.

XX N-PSDB; AAQ73749.

XX New humanised monoclonal antibodies against Human Cytomegalovirus
 PT - contain murine CDR and human framework modified to increase
 PT specificity or affinity, for treatment or prevention of HCMV
 PT infection.

XX Disclosure; Figure 2; 53pp; English.

XX

CC Human monoclonal antibodies may be made specific for a pathogen by
 CC substituting the complementarity determining regions (CDR's) from
 CC the murine antibody variable domains which show desirable binding
 CC properties to that pathogen, into the human immunoglobulin heavy and
 CC light chain variable domains. These "humanised" antibodies should
 CC elicit a considerably reduced immune response in humans compared to
 CC chimeric antibodies as they contain considerably less murine
 CC components and their half life in the circulation should approach
 CC that of natural human antibodies. This sequence is taken from a
 CC donor monoclonal antibody HCV16, specific for the human
 CC cytomegalovirus gH glycoprotein from which CDR's were taken to
 CC construct humanised antibodies. Humanised antibodies are described
 CC in AAQ63902-Q63908.
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 31; DB 15; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db | | | | | | |
 54 lasnies 60

RESULT 9
 AAR53930
 ID AAR53930 standard; Protein; 111 AA.
 XX
 AC AAR53930;
 XX
 DT 05-DEC-1994 (first entry)
 XX
 DE Light chain variable region of humanised antibody 16HuVK.

XX Antibody; humanised antibody; variable region; immune response;
 KW cytomegalovirus; glycoprotein; complementarity determining region;
 KW CDR; heavy chain; light chain.

XX Homo sapiens.
 OS Mus musculus.

XX WO9409136-A.

XX 28-APR-1994.

XX 15-OCT-1993; 93WO-GB02134.

XX 15-OCT-1992; 92GB-0021654.

XX (KETT-) KETTOK LODGE CAMPUS 2.

XX Carr FJ, Hamilton AA, Harris WJ;

XX WPI; 1994-151321/18.

XX N-PSDB; AAQ63908.

XX New humanised monoclonal antibodies against Human Cytomegalovirus
 PT - contain murine CDR and human framework modified to increase
 PT specificity or affinity, for treatment or prevention of HCMV
 PT infection.

XX Example 1; Figure 5; 53pp; English.

XX Human monoclonal antibodies may be made specific for a pathogen by
 CC substituting the complementarity determining regions (CDR's) from
 CC the murine antibody variable domains which show desirable binding
 CC properties to that pathogen, into the human immunoglobulin heavy and
 CC light chain variable domains. These "humanised" antibodies should
 CC elicit a considerably reduced immune response in humans compared to
 CC chimeric antibodies as they contain considerably less murine
 CC components and their half life in the circulation should approach

CC that of natural human antibodies. This sequence is a humanised heavy
 CC chain variable region comprising CDR's from the donor monoclonal
 CC antibody HCV16, specific for the human cytomegalovirus gH
 CC glycoprotein. The framework region of the human heavy chain has been
 CC modified. Humanised antibodies are described in AAQ63902-Q63908.
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 15; Length 111;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db | | | | | | |
 54 lasnies 60

RESULT 10
 AAR60528
 ID AAR60528 standard; Protein; 111 AA.

XX
 AC AAR60528;

XX 07-APR-1995 (first entry)

XX Light chain variable region of monoclonal antibody 5E8.

XX Secretion sequence; vector; antibody; single chain antibody;
 KW promoter; Bacillus subtilis; ss.

XX Synthetic.

XX EP614982-A.

XX 14-SEP-1994.

XX 05-MAR-1994; 94EP-0200564.

XX 10-MAR-1993; 93IT-OMI0456.

XX (ENIE) ENIRICERCH SPA.

XX Cuzzoni A, De FERRA F, Grandi G, Tortora O, Tosi C;

XX WPI; 1994-281209/35.

XX N-PSDB; AAQ71286.

XX Vector for secretion of single chain antibody from Bacillus
 PT subtilis - contg. neutral protease promoter and specific leader
 PT sequence, providing high yield of soluble antibody for diagnostic
 PT or therapeutic use

XX Example 3; Figure 2; 27pp; English.

XX The sequence encoding the variable region of the light chain of the
 CC monoclonal antibody 5E8 (specific for the alpha subunit of human
 CC gonadotropin) was amplified for its use in a recombinant vector
 CC which also comprised (1) the promoter of the gene for the neutral
 CC protease of Bacillus subtilis BGSC 1A341, (2) the secretion sequence
 CC described in AAQ71278. The amplified fragment was used to produce a
 CC DNA sequence encoding an antibody in single molecule form with the
 CC sequence VH/VK-L-VK/VH-(TAG)n, where VH and VK are the variable
 CC regions of the heavy and light chains of the antibody and L is the
 CC linker of sequence Val-Ser-Ser-(Gly(4)-Ser)3. TAG is a peptide
 CC recognised by polyclonal antibodies directed towards the same peptide,
 CC n is 1 or 0. The vector is used for the production of single chain
 CC antibodies which have improved pharmacokinetic properties and can be
 CC produced more economically than monoclonal antibodies. The vector
 CC allows production of antibodies in completely soluble form with
 CC secretion in high yield.

XX Sequence 111 AA;

Query Match 100.0%; Score 31; DB 15; Length 111;
 Best Local Similarity 100.0%; Pred. NO. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |
 Db 54 lasnles 60

RESULT 11

AAR85242
 ID AAR85242 standard; Protein; 111 AA.

XX AC AAR85242;

XX DT 09-APR-1996 (first entry)

XX DE Humanised antibody variable light chain region (VZV HuVK).

XX KW Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
 KW infection; detection; isolation; monoclonal antibody; Mab; mimetic;
 KW humanised; murine; heavy chain; light chain; variable region; CDR;
 KW NEWM; REI.

XX OS Synthetic.

XX PN W09531546-A1.

XX PD 23-NOV-1995.

XX PF 28-APR-1995; 95WO-US05305.

XX PR 28-APR-1994; 94US-0234133.

XX PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.

XX PI Carr FJ, Harris WJ, Moss MT, Wallace TP;

XX DR WPI; 1996-010932/01.

XX PT Varicella zoster virus gpIII antibody with humanised variable region
 PT - for treatment, prevention or diagnosis of varicella zoster virus
 PT infections

XX PS Claim 7; Page 31; 58pp; English.

XX CC Antibodies (Ab) comprising a humanised variable region specifically
 CC binding to a varicella zoster virus (VZV) can be used to treat or
 CC prevent vzv infection. They may optionally be attached to a
 CC therapeutic agent. They may also be used, when labelled, to detect
 CC vzv particles and infected cells in blood; for the removal/
 CC neutralisation of infectious vzv in blood; for the selection/
 CC isolation of human monoclonal Abs and for the design of (non-)
 CC peptide mimetics with similar diagnostic and therapeutic uses. The
 CC variable region CDR portion is derived from murine Ab 206 and the
 CC heavy and light chain variable region frameworks are NEWM and REI
 CC respectively. The framework may include at least one mutation that
 CC improves binding specificity or affinity. The heavy and light chain
 CC variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY,
 CC -VHKVRSE or -VHS) and VZVHuVK respectively.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 17; Length 111;
 Best Local Similarity 100.0%; Pred. NO. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |
 Db 54 lasnles 60

RESULT 12

AAR85236
 ID AAR85236 standard; Protein; 111 AA.

XX AC AAR85236;

XX DT 05-APR-1996 (first entry)

XX DE Murine 206 antibody variable light chain region.

XX KW Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
 KW infection; detection; isolation; monoclonal antibody; Mab; mimetic;
 KW humanised; murine; heavy chain; light chain; variable region; CDR;
 KW NEWM; REI.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX FT Binding-site 24..38

XX FT Binding-site /label= CDR 1.

XX FT Binding-site 54..60

XX FT Binding-site /label= CDR 2.

XX FT Binding-site 93..101

XX FT Binding-site /label= CDR 3.

XX PN W09531546-A1.

XX PD 23-NOV-1995.

XX PF 28-APR-1995; 95WO-US05305.

XX PR 28-APR-1994; 94US-0234133.

XX PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.

XX PI Carr FJ, Harris WJ, Moss MT, Wallace TP;

XX DR WPI; 1996-010932/01.

XX DR N-PSDB; AAT06051.

XX PT Varicella zoster virus gpIII antibody with humanised variable region
 PT - for treatment, prevention or diagnosis of varicella zoster virus
 PT infections

XX PS Claim 2; Figure 2; 58pp; English.

XX CC Antibodies (Ab) comprising a humanised variable region specifically
 CC binding to a varicella zoster virus (VZV) can be used to treat or
 CC prevent vzv infection. They may optionally be attached to a
 CC therapeutic agent. They may also be used, when labelled, to detect
 CC vzv particles and infected cells in blood; for the removal/
 CC neutralisation of infectious vzv in blood; for the selection/
 CC isolation of human monoclonal Abs and for the design of (non-)
 CC peptide mimetics with similar diagnostic and therapeutic uses. The
 CC variable region CDR portion is derived from murine Ab 206 and the
 CC heavy and light chain variable region frameworks are NEWM and REI
 CC respectively. The framework may include at least one mutation that
 CC improves binding specificity or affinity. The heavy and light chain
 CC variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY,
 CC -VHKVRSE or -VHS) and VZVHuVK respectively.

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 31; DB 17; Length 111;
 Best Local Similarity 100.0%; Pred. NO. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |
 Db 54 lasnles 60

RESULT 13

AAW89351

ID AAW89351 standard; Protein; 111 AA.

XX AC AAW89351;

XX DT 02-MAR-1999 (first entry)

XX DE Humanised 23F2G light chain variable region.

XX KW Mouse; humanised; antibody; heavy chain variable region; light chain;
 XX KW 23F2G; inflammatory disease; multiple sclerosis; common beta chain;
 XX KW CD18; human leukocyte integrin.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US5854070-A.

XX PD 29-DEC-1998.

XX PF 21-JAN-1997; 97US-0785571.

XX PR 16-JUL-1993; 93US-0094535.

XX PR 16-JUL-1992; 92US-0915068.

XX PR 10-MAY-1993; 93US-0060699.

XX PR 28-FEB-1995; 95US-0396089.

XX PR 21-JAN-1997; 97US-0785571.

XX PA (ICOS-) ICOS CORP.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Rose LM;

XX DR WPI; 1999-094920/08.

XX DR N-PSDB; AAV81909.

XX DT Hybridomas that secrete anti-CD18 antibody - useful for treating
 XX PT Inflammation specifically multiple sclerosis
 XX PS Example 6; Column 27-30; 24pp; English.

XX SQ Sequence 111 AA;

Query Match

Best Local Similarity 100.0%; Score 31; DB 20; Length 111;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7

Db 54 lasnles 60

RESULT 14

AAB10019

ID AAB10019 standard; Protein; 111 AA.

XX AC AAB10019;

XX DT 01-NOV-2000 (first entry)

XX DE

DE

XX

KW

KW

XX

OS

XX

PN

XX

PD

XX

XX

PF

XX

PR

PR

XX

XX

PA

XX

PI

XX

XX

DR

DR

XX

XX

PT

PT

XX

XX

PS

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XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

H. pylori HSP60-binding antibody light chain protein.

Acid-resistant microorganism; detection; faecal; intestine; infection;
 monoclonal antibody; heat shock protein; HSP60; light chain.

Unidentified.

WO200026671-A1.

11-MAY-2000.

29-OCT-1999; 99WO-EP08212.

29-OCT-1998; 98EP-0120517.

06-NOV-1998; 98EP-0120687.

(CONN-) CONNEX GMBH.

Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
Ringeis A;

WPI; 2000-365747/31.

N-PSDB; AAA40199.

Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 pylori, comprises reacting a faecal sample with two binding reagents for
 antigens that survive intestinal passage -

Disclosure; Fig 1; 84pp; German.

This invention describes a novel method for the detection of a mammalian
 infection by an acid-resistant microorganism (A) by treating a faecal
 sample with at least two different monoclonal antibodies (MAB) (or their
 fragments or derivatives) or aptamers (collectively (I)) and detecting
 formation of a complex (C) between (I) and the corresponding antigen of
 (A). The first and second (I) bind to epitopes of different antigens
 (Ag). These epitopes are present, after passage through the intestines,
 in at least some mammals, and have either: (i) their native structure;
 or (ii) a structure against which an antibody is produced by an animal
 infected or immunized with (A), or its extract, lysate, derived protein
 or fragment, or with a synthetic peptide. Practically all mammals display
 at least one of the specified epitopes. The method is used to detect
 infection by acid-fast bacteria, particularly of the genera Helicobacter,
 Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 therapeutically. The method is direct and non-invasive, and provides an
 inexpensive and easily standardizable diagnosis, despite possible
 degradation of antigens during passage through the intestines. This
 sequence represents the H. pylori heat shock protein, HSP60-binding
 antibody (DMS ACC2356) light chain which is used to illustrate the method
 of the invention.

SQ Sequence 111 AA;

Query Match

Best Local Similarity 100.0%; Score 31; DB 21; Length 111;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7

Db 54 lasnles 60

RESULT 15

AAR10539

ID AAR10539 standard; Protein; 112 AA.

XX AC AAR10539;

XX DT 15-APR-1991 (first entry)

XX DE Chimeric MAB 9.2.27 light chain variable region.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:15 ; Search time 138.34 Seconds
(without alignments)
1.019 Million cell updates/sec

Title: US-09-724-406-30
Perfect score: 31
Sequence: 1 LASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
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6: /cgn2.6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	100.0	17	2	US-08-712-212-5
2	31	100.0	17	5	PCT-US95-05160-5
3	31	100.0	111	1	US-08-207-169A-4
4	31	100.0	130	1	US-08-137-117D-86
5	31	100.0	130	2	US-08-436-717-86
6	31	100.0	131	1	US-08-137-117D-25
7	31	100.0	131	2	US-08-436-717-25
8	28	90.3	91	2	US-08-273-146-49
9	28	90.3	110	1	US-08-017-570-2
10	28	90.3	110	1	US-08-471-426-2
11	28	90.3	110	5	PCT-US94-01709-2
12	28	90.3	111	1	US-08-111-080-30
13	28	90.3	111	1	US-08-111-080-32
14	28	90.3	111	1	US-08-273-053-11
15	28	90.3	111	1	US-08-273-053-14
16	28	90.3	111	1	US-08-211-980-30
17	28	90.3	111	1	US-08-211-980-32
18	28	90.3	111	5	PCT-US93-07967-30
19	28	90.3	111	5	PCT-US93-07967-32
20	28	90.3	121	1	US-08-111-080-18
21	28	90.3	121	1	US-08-111-080-22
22	28	90.3	121	1	US-08-211-980-18
23	28	90.3	121	1	US-08-211-980-22
24	28	90.3	121	5	PCT-US92-07111-17
25	28	90.3	121	5	PCT-US93-07967-18
26	28	90.3	121	5	PCT-US93-07967-22
27	28	90.3	1618	4	US-08-462-467B-4

28 28 90.3 2887 4 US-08-462-467B-2 Sequence 2, Appli
29 28 90.3 2887 4 US-08-462-467B-8 Sequence 8, Appli
30 27 87.1 6 1 US-08-137-117D-137 Sequence 137, App
31 27 87.1 6 2 US-08-436-717-137 Sequence 137, App
32 27 87.1 7 1 US-08-318-970B-16 Sequence 16, Appl
33 27 87.1 7 2 US-08-483-635-18 Sequence 18, Appl
34 27 87.1 7 2 US-08-483-632-18 Sequence 18, Appl
35 27 87.1 37 4 US-08-767-128-40 Sequence 40, Appl
36 27 87.1 41 3 US-08-984-277-6 Sequence 6, Appli
37 27 87.1 64 2 US-08-765-179B-10 Sequence 10, Appl
38 27 87.1 106 1 US-08-202-047-26 Sequence 26, Appl
39 27 87.1 106 3 US-08-964-690-26 Sequence 26, Appl
40 27 87.1 106 3 US-08-466-151-6 Sequence 6, Appli
41 27 87.1 110 1 US-08-442-542-8 Sequence 8, Appli
42 27 87.1 110 3 US-08-483-749A-20 Sequence 20, Appl
43 27 87.1 110 3 US-08-765-469-8 Sequence 8, Appli
44 27 87.1 111 1 US-07-634-278-46 Sequence 46, Appl
45 27 87.1 111 1 US-07-634-278-47 Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-712-212-5
; Sequence 5, Application US/08712212
; Patent No. 5837460
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Vonfeldt, Joan M.
; TITLE OF INVENTION: Biologically active peptides and
; TITLE OF INVENTION: methods of identifying the same
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5837460ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,212
; FILING DATE: 03-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,404
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-1554
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-712-212-5

Query Match 100.0%; Score 31; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LASNLES 7
| | | | |
DB 2 LASNLES 8

RESULT 2

PCT-US95-05160-5
; Sequence 5, Application PC/TUS9505160
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Vonfeldt, Joan M.
; TITLE OF INVENTION: Biologically active peptides and
; TITLE OF INVENTION: methods of identifying the same
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05160
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,404
; FILING DATE: 29-APR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2245
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05160-5

Query Match 100.0%; Score 31; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

OY 1 LASNLES 7
| | | | |
DB 2 LASNLES 8

RESULT 3

US-08-207-169A-4
; Sequence 4, Application US/08207169A
; Patent No. 5674712
; GENERAL INFORMATION:
; APPLICANT: GRANDI, GUIDO
; APPLICANT: DE FERRA, FRANCESCA
; APPLICANT: TOSI, CLAUDIO
; APPLICANT: TORTORA, ORNELLA

; APPLICANT: CUZZONI, ANNA
; TITLE OF INVENTION: RECOMBINANT VECTOR AND USE THEREOF FOR
; TITLE OF INVENTION: EXOCYLLULAR PREPARATION OF SINGLE MOLECULA ANTIBODIES FROM
; TITLE OF INVENTION: BACILLUS SUBTILIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,169A
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5674712man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2264-061-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-207-169A-4

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LASNLES 7
| | | | |
DB 54 LASNLES 60

RESULT 4

US-08-137-117D-86
; Sequence 86, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-137-117D-86

Query Match 100.0%; Score 31; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 73 LASNLES 79

RESULT 5
US-08-436-717-86
; Sequence 86, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-717-86

Query Match 100.0%; Score 31; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 73 LASNLES 79

RESULT 6
US-08-137-117D-25
; Sequence 25, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-25

Query Match 100.0%; Score 31; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 74 LASNLES 80

RESULT 7
US-08-436-717-25
Sequence 25, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-25

Query Match 100.0%; Score 31; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 74 LASNLES 80

RESULT 8
US-08-273-146-49
Sequence 49, Application US/08273146
Patent No. 5855885
GENERAL INFORMATION:
APPLICANT: Smith, Rodger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
APPLICANT: Darsley, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-49

Query Match 90.3%; Score 28; DB 2; Length 91;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 46 LASNLES 52


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RESULT 9
US-08-017-570-2
; Sequence 2, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-017-570-2

Query Match 90.3%; Score 28; DB 1; Length 110;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 54 LASNLQS 60
|||||:1

RESULT 10
US-08-471-426-2
; Sequence 2, Application US/08471426
; Patent No. 5806033
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US

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; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-426-2

Query Match 90.3%; Score 28; DB 1; Length 110;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 54 LASNLQS 60
|||||:1

RESULT 11
PCT-US94-01709-2
; Sequence 2, Application PC/TUS9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

MOLECULE TYPE: protein
PCT-US94-01709-2

Query Match 90.3%; Score 28; DB 5; Length 110;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 54 VASNLES 60

RESULT 12
US-08-111-080-30
; Sequence 30, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-080-30

Query Match 90.3%; Score 28; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 54 VASNLES 60

RESULT 13
US-08-111-080-32
; Sequence 32, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-111-080-32

Query Match 90.3%; Score 28; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 54 VASNLES 60

RESULT 14
US-08-275-053-11
; Sequence 11, Application US/08275053
; Patent No. 5607847
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
; virus antibody.
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,053
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/01798
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-275-053-11

Query Match 90.3%; Score 28; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

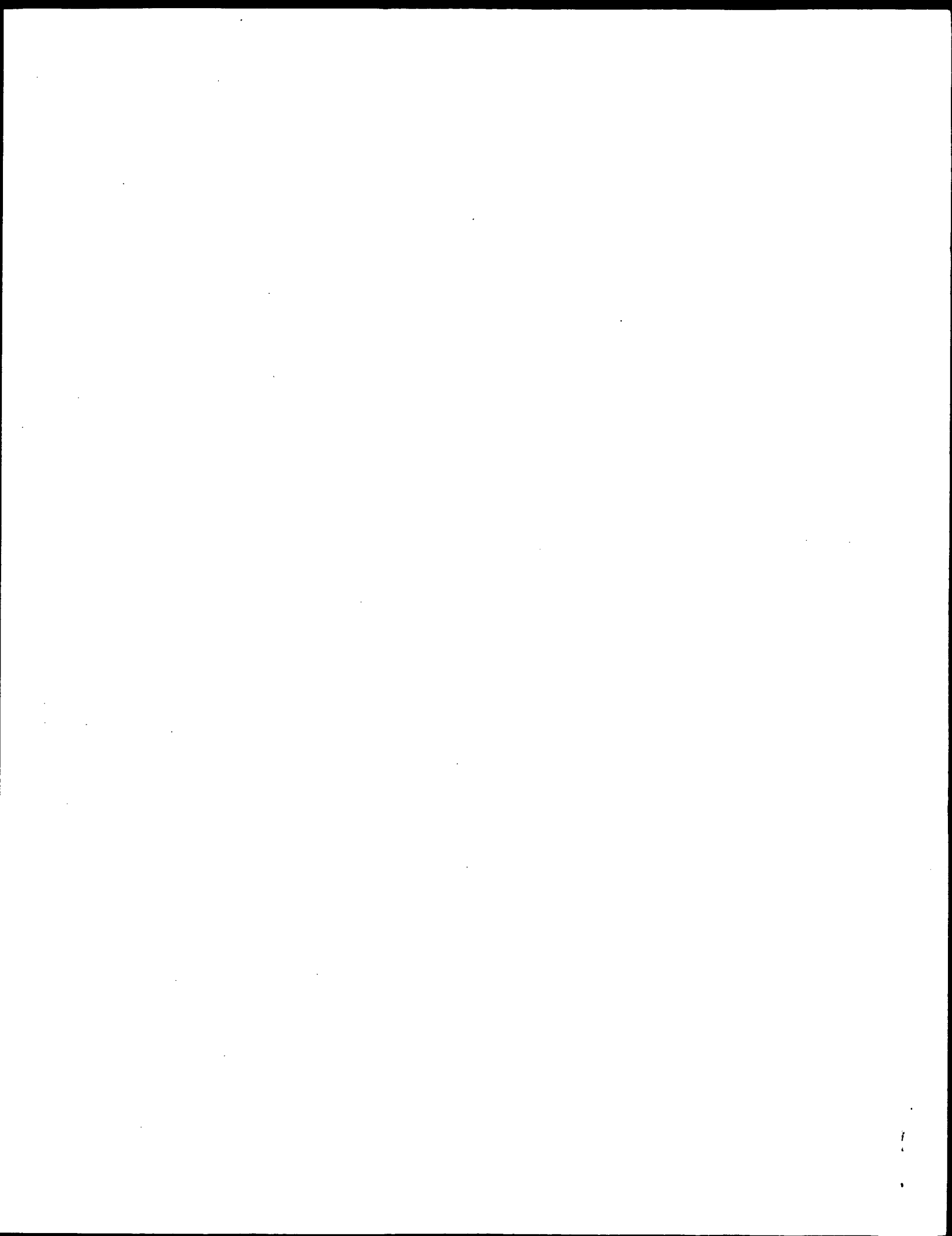
Qy 1 LASNLES 7
Db 54 VASNLES 60

RESULT 15
US-08-275-053-14
; Sequence 14, Application US/08275053
; Patent No. 5607847
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
; TITLE OF INVENTION: virus antibody.
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/08/275,053
; APPLICATION NUMBER: US/08/275,053
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/01798
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-275-053-14

Query Match 90.3%; Score 28; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 54 VASNLES 60

Search completed: June 28, 2001, 16:01:15
Job time: 523 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:46 ; Search time 234.85 Seconds
(without alignments)
2.270 Million cell updates/sec

Title: US-09-724-406-30
Perfect score: 31
Sequence: 1 LASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	95	2 S25177	Ig kappa chain V r
2	31	100.0	102	2 PH1076	Ig light chain V r
3	31	100.0	111	1 KVM584	Ig kappa chain V r
4	31	100.0	111	1 KVM575	Ig kappa chain V r
5	31	100.0	111	1 KVM540	Ig kappa chain V r
6	31	100.0	111	2 D45722	anti-glycoprotein
7	31	100.0	112	2 S45715	Ig kappa chain V r
8	31	100.0	131	1 KVM5M6	Ig kappa chain pre
9	31	100.0	210	2 A56169	Ig kappa chain V r
10	31	100.0	218	2 JC5810	monoclonal antibod
11	29	93.5	94	2 PS0349	myosin heavy chain
12	29	93.5	230	1 UVFUS	cutinase (EC 3.1.-
13	29	93.5	741	2 S39082	myosin heavy chain
14	29	93.5	936	2 S39083	myosin heavy chain
15	29	93.5	955	2 S24348	myosin heavy chain
16	29	93.5	1938	1 JX0178	myosin heavy chain
17	29	93.5	1940	2 A29320	myosin heavy chain
18	28	90.3	81	2 S42193	Ig kappa chain V r
19	28	90.3	186	2 H75004	hypothetical prote
20	28	90.3	186	2 A71158	hypothetical prote
21	28	90.3	218	2 S68241	Ig kappa chain V r
22	28	90.3	367	2 T28892	hypothetical prote
23	28	90.3	376	2 T19266	hypothetical prote
24	28	90.3	1116	2 S63397	probable membrane
25	28	90.3	1225	1 B64234	hypothetical prote
26	28	90.3	1549	2 S50705	hypothetical prote
27	27	87.1	65	2 C38601	Ig kappa chain V r
28	27	87.1	65	2 B38601	Ig kappa chain V r
29	27	87.1	91	2 S25462	Ig kappa chain V r

```

30 27 87.1 93 2 A38601 Ig kappa chain V r
31 27 87.1 101 2 S59640 Ig light chain V r
32 27 87.1 102 2 PC6027 acetylcholine recep
33 27 87.1 102 2 PH1077 Ig light chain V r
34 27 87.1 107 2 S26343 Ig kappa chain V r
35 27 87.1 107 2 S26344 Ig kappa chain V r
36 27 87.1 108 1 K1HUAU Ig kappa chain V-I
37 27 87.1 108 1 KVM554 Ig kappa chain V r
38 27 87.1 108 2 PH0092 Ig kappa chain V r
39 27 87.1 110 1 KVM510 Ig kappa chain V r
40 27 87.1 110 2 S24288 Ig kappa chain V r
41 27 87.1 111 1 KVM537 Ig kappa chain V r
42 27 87.1 111 1 KVM5C1 Ig kappa chain V r
43 27 87.1 111 1 KVM543 Ig kappa chain V r
44 27 87.1 111 1 KVM583 Ig kappa chain V r
45 27 87.1 111 1 KVM508 Ig kappa chain V r

```

ALIGNMENTS

RESULT 1

S25177
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S25177; S33134
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
A:Description: Structure and binding properties of monoclonal antibodies to core hist
A:Reference number: S25174
A:Accession: S25177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95 <MON>
A:Cross-references: EMBL:X67625; NID:g52146; PIDN:CAA47883.1; PID:g938262
A:Accession: S33134
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95 <MO2>
A:Cross-references: EMBL:X67625; NID:g52146; PIDN:CAA47883.1; PID:g938262
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
DB 53 LASNLES 59

RESULT 2

PH1076
Ig light chain V region (clone 74-c2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1076
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1076
A:Molecule type: mRNA
A:Residues: 1-102 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 54 LASNLES 60

RESULT 3
 KVM584
 Ig kappa chain V region (PC6684) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
 C:Accession: A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 54 LASNLES 60

RESULT 4
 KVM575
 Ig kappa chain V region (PC7175) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
 C:Accession: B01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 54 LASNLES 60

RESULT 5
 KVM540
 Ig kappa chain V region (PC7940) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
 C:Accession: C01938; A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: C01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 54 LASNLES 60

RESULT 6
 D45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: D45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: D45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-111 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120592)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 54 LASNLES 60

RESULT 7
 S45715
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
 C:Accession: S45715
 R:Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi,
 FEBS Lett. 346, 246-250, 1994
 A:Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen
 A:Reference number: S45714; MUID:94283606
 A:Accession: S45715
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-112 <KIM>
 A:Experimental source: cell line Ex-3C7
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 LASNLES 7
| | | | |
Db 54 LASNLES 60

RESULT 8

KVMSM6

Ig kappa chain precursor V regions (M63, AB22, PC9245, PC4050) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: B90412; B90374; B93822; C93204; D93204; PH1078; A01935
R:Burstein, Y.; Schechter, I.
Biochemistry 17, 2392-2400, 1978
A:Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.
A:Reference number: A90412; MUID:78235887
A:Contents: M63
A:Accession: B90412
A:Molecule type: protein
A:Residues: 1-35 <BUR>
R:McKean, D.; Potter, M.; Hood, L.
Biochemistry 12, 760-771, 1973
A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains
A:Reference number: A90374; MUID:73140225
A:Contents: M63
A:Accession: B90374

A:Molecule type: protein
A:Residues: 21-46,'Q',48-53,'B',55-57,'Z',59-86,'F',88-131 <MCK>
A:Note: this sequence has since been revised in reference A93822
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo
A:Reference number: A93822; MUID:79012520
A:Contents: M63; AB22
A:Accession: B93822
A:Molecule type: protein
A:Residues: 1-53;59-107 <MC2>
A:Accession: C93822
A:Molecule type: protein
A:Residues: 21-119,'Y',121-131 <MC3>
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Contents: PC9245; PC4050
A:Accession: C93204
A:Molecule type: protein
A:Residues: 21-119,'Y',121-131 <WE1>
A:Accession: D93204

A:Molecule type: protein
A:Residues: 21-119,'L',121-123,'A',125-129,'L',131 <WE2>
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:93381444
A:Accession: PH1078
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 21-122 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1, clone 17p.73
C:Comment: The M63 precursor sequence is shown.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>
F:43-112/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 LASNLES 7
| | | | |
Db 74 LASNLES 80

RESULT 9

A56169

Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R:Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God
J. Biol. Chem. 270, 6628-6638, 1995
A:Title: Recombinant antibodies in bioactive peptide design.
A:Reference number: A56169; MUID:95204454
A:Accession: A56169
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-210 <MON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 LASNLES 7
| | | | |
Db 54 LASNLES 60

RESULT 10

JC5810

monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp
A:Reference number: JC5810; MUID:98063277
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 LASNLES 7
| | | | |
Db 54 LASNLES 60

RESULT 11

PS0349

myosin heavy chain, pectoralis profundus - chicken (fragments)

C:Species: Gallus gallus (chicken)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Feb-1998
 C:Accession: PS0349
 R:Matsuzono, K.; Nagata, S.; Ichikawa, M.; Matsuda, G.
 Nagasaki Igakkai Zasshi 66, 311-322, 1991
 A:Title: Structural analysis of the chicken myosin heavy chain (comparison M. pectoralis)
 A:Reference number: PS0349
 A:Accession: PS0349
 A:Molecule type: protein
 A:Residues: 1-94 <MAT>
 A:Experimental source: adult
 A:Note: article in Japanese
 A:Note: this peptide is obtained from rod portion
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP

Query Match 93.5%; Score 29; DB 2; Length 94;
 Best Local Similarity 85.7%; Pred. No. 5.6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 63 LASNIES 69

RESULT 12
 UVFUS
 C:Species: Fusarium solani f.sp. pisi
 C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 11-Jun-1999
 C:Accession: A32836; A00731; A61421
 R:Soliday, C.L.; Dickman, M.B.; Kolattukudy, P.E.
 J. Bacteriol. 171, 1942-1951, 1989
 A:Title: Structure of the cutinase gene and detection of promoter activity in the 5'-fla
 A:Reference number: A32836; MUID:89197761
 A:Accession: A32836
 A:Molecule type: DNA
 A:Residues: 1-47, 'A', 49-93, 'A', 95-230 <S01>
 A:Cross-references: GB:M29759; NID:g168147; PIDN:AAA33335.1; PID:g168148
 A:Note: the authors translated the codon GCA for residue 94 as Arg
 R:Soliday, C.L.; Flurkey, W.H.; Okita, T.W.; Kolattukudy, P.E.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3939-3943, 1984
 A:Title: Cloning and structure determination of cDNA for cutinase, an enzyme involved in
 A:Reference number: A00731
 A:Accession: A00731
 A:Molecule type: mRNA
 A:Residues: 1-230 <S02>
 A:Cross-references: GB:X02640; NID:g168145; PIDN:AAA33334.1; PID:g168146
 A:Accession: B00731
 A:Molecule type: protein
 A:Residues: 57-94; 113-142; 183-192 <S03>
 R:Soliday, C.L.; Kolattukudy, P.E.
 Biochem. Biophys. Res. Commun. 114, 1017-1022, 1983
 A:Title: Primary structure of the active site region of fungal cutinase, an enzyme invol
 A:Reference number: A61421; MUID:83308716
 A:Accession: A61421
 A:Molecule type: protein
 A:Residues: 113-142 <S04>
 R:Lin, T.S.; Kolattukudy, P.E.
 Eur. J. Biochem. 106, 341-351, 1980
 A:Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and
 A:Reference number: A44665; MUID:80245930
 A:Contents: annotation; identification of glucuronylated amino end
 C:Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str
 C:Comment: Southern blot results suggest that the genome contains two copies of the cuti
 C:Genetics:
 A:Introns: 64/3
 C:Superfamily: cutinase
 C:Keywords: blocked amino end; glycoprotein; hydrolase
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-230/Product: cutinase #status predicted <MAT>
 F:332/Modified site: glucuronylated amino end (Gly) (in mature form) #status experimental

F:125-187/Bisulfide bonds: #status experimental
 F:136,204/Active site: Ser, His #status experimental

Query Match 93.5%; Score 29; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 71 IASNLES 77

RESULT 13
 S39082
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999
 C:Accession: S39082; S24349; A30170; S01265
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o
 A:Reference number: S39081
 A:Accession: S39082
 A:Molecule type: mRNA
 A:Residues: 1-741 <MOO>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cemb3
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isof
 A:Reference number: S24348; MUID:92309413
 A:Accession: S24349
 A:Molecule type: mRNA
 A:Residues: 1-12, 14-741 <MOO2>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cemb3
 R:Lagrutta, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
 DNA 8, 39-50, 1989
 A:Title: Identification and developmental expression of a novel embryonic myosin heav

A:Reference number: A30170; MUID:89210285
 A:Accession: A30170
 A:Molecule type: DNA
 A:Residues: 723-741 <LAG>
 A:Cross-references: GB:M24691; NID:g341219; PIDN:AAA48950.1; PID:g531186
 R:McCarthy, J.G.; Heywood, S.M.
 Nucleic Acids Res. 15, 8069-8085, 1987
 A:Title: A long polypyrimidine/polypurine tract induces an altered DNA conformation o
 A:Reference number: S01265; MUID:88040428
 A:Accession: S01265
 A:Molecule type: DNA
 A:Residues: 723-741 <MCC>
 A:Cross-references: EMBL:X06251; NID:g63600; PIDN:CAA29593.1; PID:g63601
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; muscle

Query Match 93.5%; Score 29; DB 2; Length 741;
 Best Local Similarity 85.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 DB 36 LASNMES 42

RESULT 14
 S39083
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
 C:Accession: S39083; S24350; A26821
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization of isoform
 A:Reference number: S39081
 A:Accession: S39083
 A:Molecule type: mRNA
 A:Residues: 1-936 <MOO1>
 A:Cross-references: EMBL:M74087
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
 A:Reference number: S24348; MUID:92309413
 A:Accession: S24350
 A:Molecule type: mRNA
 A:Residues: 3-466, 'O', 468-641, 'R', 643-936 <MOO2>
 A:Cross-references: EMBL:M74087
 R:Worliarity, D.M.; Barringer, K.J.; Dodgson, J.B.; Richter, H.E.; Young, R.B.
 DNA 6, 91-99, 1987
 A:Title: Genomic clones encoding chicken myosin heavy-chain genes.
 A:Reference number: A26821; MUID:87217964
 A:Accession: A26321
 A:Molecule type: DNA
 A:Residues: 'F', 856-936 <WOR>
 A:Cross-references: GB:M16557; NID:9212371; PIDN:AAA48970.1; PID:9212372
 C:Genetics:
 A:Introns: 886/3
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match 93.5%; Score 29; DB 2; Length 936;
 Best Local Similarity 85.7%; Pred. NO. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||

Db 232 LASNMES 238

RESULT 15

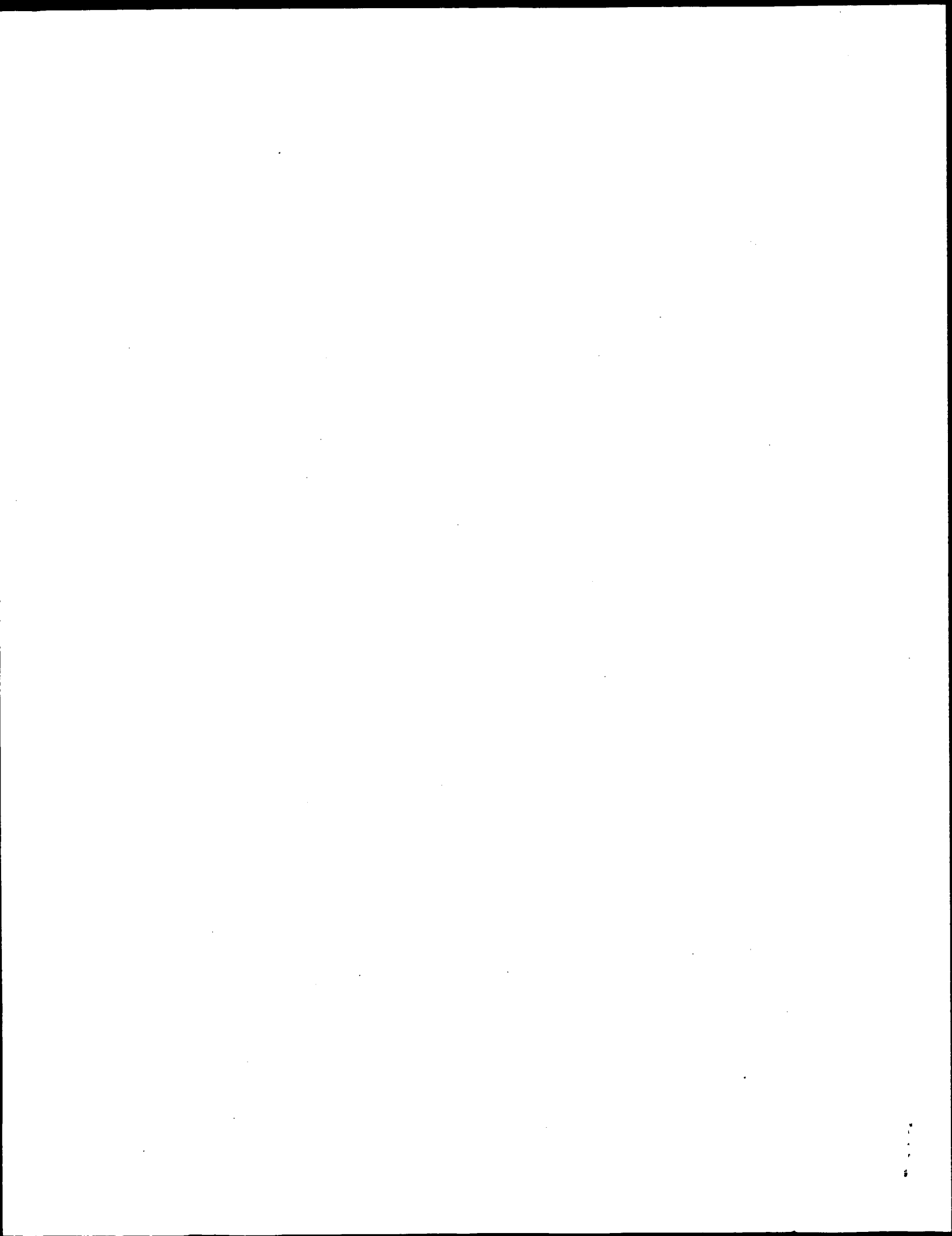
S24348
 myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
 C:Accession: S24348
 R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
 A:Reference number: S24348; MUID:92309413
 A:Accession: S24348
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-955 <MOO>
 A:Cross-references: EMBL:M74085
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match 93.5%; Score 29; DB 2; Length 955;
 Best Local Similarity 85.7%; Pred. NO. 73;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||

Db 250 LASNMES 256

Search completed: June 28, 2001, 15:58:46
 Job time: 374 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:39 ; Search time 105.36 Seconds
(without alignments)
2.276 Million cell updates/sec

Title: US-09-724-406-30
Perfect score: 31
Sequence: 1 LASNLES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	111	1 KV3J_MOUSE	P01662 mus musculus
2	31	100.0	111	1 KV3K_MOUSE	P01663 mus musculus
3	31	100.0	111	1 KV3R_MOUSE	P01670 mus musculus
4	31	100.0	111	1 KV3S_MOUSE	P01671 mus musculus
5	31	100.0	111	1 KV3T_MOUSE	P01672 mus musculus
6	31	100.0	131	1 KV3L_MOUSE	P01661 mus musculus
7	29	93.5	230	1 CUTI_FUSSC	Q99174 fusarium so
8	29	93.5	230	1 CUTI_FUSSO	P00590 fusarium so
9	29	93.5	1938	1 MYSS_CHICK	P13538 gallus gall
10	29	93.5	1940	1 MYSE_CHICK	P02565 gallus gall
11	28	90.3	186	1 NADM_PVRAB	Q9uyd4 pyrococcus
12	28	90.3	186	1 NADM_PVRHO	O58211 pyrococcus
13	28	90.3	376	1 KYVA_CAEEL	Q17963 caenorhabdi
14	28	90.3	1116	1 IN94_YEAST	P53751 saccharomyc
15	28	90.3	1225	1 Y309_MYCGE	P47551 mycoplasma
16	28	90.3	1549	1 Y309_YEAST	P40438 saccharomyc
17	28	90.3	1549	1 YJW2_YEAST	P40890 saccharomyc
18	27	87.1	108	1 KV1B_HUMAN	P01594 homo sapien
19	27	87.1	108	1 KV3V_MOUSE	P01674 mus musculus
20	27	87.1	110	1 KV3P_MOUSE	P01668 mus musculus
21	27	87.1	111	1 KV3H_MOUSE	P01660 mus musculus
22	27	87.1	111	1 KV3L_MOUSE	P01664 mus musculus
23	27	87.1	111	1 KV3M_MOUSE	P01665 mus musculus
24	27	87.1	111	1 KV3N_MOUSE	P01666 mus musculus
25	27	87.1	111	1 KV3O_MOUSE	P01667 mus musculus
26	27	87.1	111	1 KV3Q_MOUSE	P01669 mus musculus
27	27	87.1	155	1 Y359_RICPR	Q9zdg9 rickettsia
28	27	87.1	323	1 RFC4_YEAST	P40339 saccharomyc
29	27	87.1	463	1 YIEQ_HAEIN	P44903 haemophilus
30	27	87.1	714	1 YFE7_YEAST	P43556 saccharomyc
31	27	87.1	1325	1 Y309_MYCPN	P75334 mycoplasma
32	26	83.9	111	1 KV3U_MOUSE	P01673 mus musculus
33	26	83.9	112	1 KV3G_MOUSE	P01659 mus musculus

34	26	83.9	132	1 KV3F_MOUSE	P01658 mus musculus
35	26	83.9	257	1 LSG4_HAEIN	P71398 haemophilus
36	26	83.9	258	1 Y875_SYNY3	P73555 synechocyst
37	26	83.9	648	1 KAPC_DICDI	P34099 dictyostell
38	26	83.9	796	1 MBN_DROME	P52302 drosophila
39	26	83.9	876	1 MYSS_HUMAN	P12882 homo sapien
40	25	80.6	146	1 RS18_YEAST	P35271 saccharomyc
41	25	80.6	175	1 CSF3_CANFA	P35934 canis famli
42	25	80.6	191	1 YDA4_SCHPO	Q10346 schizosacch
43	25	80.6	193	1 VIN3_BPT4	P13302 bacterioph
44	25	80.6	194	1 CSF3_FELCA	Q02708 felis silve
45	25	80.6	197	1 YQOC_CAEEL	Q09301 caenorhabdi

ALIGNMENTS

RESULT 1
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gattaman L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
CC -!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM5M6.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.78; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0

QY 1 LASNLES 7
Db 54 LASNLES 60

RESULT 2
KV3K_MOUSE
ID KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 4050.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01935; KWSM6.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 54 LASNLES 60

RESULT 3
KV3R_MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 6684.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01938; KWSM84.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; 1E4698834185826 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 54 LASNLES 60

RESULT 4
KV3S_MOUSE
ID KV3S_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7175.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: B01938; KWSM75.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASNLES 7
Db 54 LASNLES 60

RESULT 5
KV3T_MOUSE
ID KV3T_MOUSE STANDARD; PRT; 111 AA.
AC P01672;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7940.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";

```

FT DOMAIN 122 131 FRAMEWORK 4.
FT FT DISULFID 43 112 BY SIMILARITY.
FT FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 100.0%; Score 31; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LASNLES 7
DB 74 LASNLES 80

RESULT 7
CUT1_FUSSC
ID CUT1_FUSSC STANDARD; PRT; 230 AA.
AC Q99174;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CUTINASE PRECURSOR (EC 3.1.1.-).
GN CUTA.
OS Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=57162;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PGB 153;
RC MEDLINE=9725498; PubMed=9100380;
RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
RA Rees-George J., Rikkerink E.H., Templeton M.D.;
RT "Effect of disruption of a cutinase gene (cutA) on virulence and
RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
RT Cucurbita maxima and C. moschata.";
RL Mol. Plant Microbe Interact. 10:355-368(1997).
CC -!- FUNCTION: ALLOWS PATHOGENIC FUNGI TO PENETRATE THROUGH THE
CC CUTICULAR BARRIER INTO THE HOST PLANT DURING THE INITIAL STAGE
CC OF THE FUNGAL INFECTION (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF CUTIN, A POLYESTER THAT
CC FORMS THE STRUCTURE OF PLANT CUTICLE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
CC EMBL; U63335; AA805922.1; -.
CC HSP; P00590; 2CUT.
CC InterPro; IPR000675; -.
CC Pfam; PF01083; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; P500155; CUTINASE_1; 1.
CC PROSITE; P500931; CUTINASE_2; 1.
CC Hydroxylase; Serine esterase; Glycoprotein; Signal.
CC SIGNAL 1 16 BY SIMILARITY.
CC CHAIN 17 230 CUTINASE.
CC FT DISULFID 47 194 BY SIMILARITY.
CC FT DISULFID 125 187 BY SIMILARITY.
CC FT ACT_SITE 136 136 BY SIMILARITY.
CC FT ACT_SITE 191 191 BY SIMILARITY.
CC FT ACT_SITE 204 204 BY SIMILARITY.

```

SQ SEQUENCE 230 AA; 23902 MW; 05FB3C3326405AA CRC64;
 Query Match 93.5%; Score 29; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 5.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASNLES 7
 :|||||
 Db 71 IASNLES 77
 RESULT 8
 ID CUTI_FUSSO STANDARD; PRT; 230 AA.
 AC P00590; 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CUTINASE PRECURSOR (EC 3.1.1.-).
 GN CUTA.
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).
 OC Eukaryota; Fungi; Ascomycota; Mitosporic Ascomycota; Fusarium.
 OX NCBI_TaxID=109625;
 RN (1)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-T-8;
 RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;
 RT "Cloning and structure determination of cDNA for cutinase, an enzyme
 involved in fungal penetration of plants.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89197761; PubMed=2703464;
 RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;
 RT "Structure of the cutinase gene and detection of promoter activity in
 the 5'-flanking region by fungal transformation.";
 RL J. Bacteriol. 171:1942-1951(1989).
 RN (3)
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=92220194; PubMed=1560844;
 RA Martinez C., de Geus P., Lauwereys M., Matthysens G., Cambillau C.;
 RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
 serine accessible to solvent.";
 RL Nature 356:615-618(1992).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=94114517; PubMed=8286366;
 RA Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey C.,
 Verger R., Cambillau C.;
 RT "Cutinase, a lipolytic enzyme with a preformed oxyanion hole.";
 RL Biochemistry 33:83-89(1994).
 RN (5)
 RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).
 RX MEDLINE=97318923; PubMed=9175860;
 RA Longhi S., Czjzek M., Lamzin V., Nicolas A., Cambillau C.;
 RT "Atomic resolution (1.0 Å) crystal structure of Fusarium solani
 cutinase: stereochemical analysis.";
 RL J. Mol. Biol. 268:779-799(1997).
 RN (6)
 RP X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230.
 RA Nicolas A., Martinez C., Cambillau C.;
 RL Submitted (MAR-1997) to the PDB data bank.
 RN (7)
 RP STRUCTURE BY NMR.
 RX MEDLINE=98046750; PubMed=9385640;
 RA Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.,
 Hilbers C.W.;
 RT "1H, 13C, and 15N resonance assignments of Fusarium solani pisi
 cutinase and preliminary features of the structure in solution.";
 RL Protein Sci. 6:2375-2384(1997).
 CC -1- FUNCTION: ALLOWS PATHOGENIC FUNGI TO PENETRATE THROUGH THE
 CUTICULAR BARRIER INTO THE HOST PLANT DURING THE INITIAL STAGE

CC OF THE FUNGAL INFECTION.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF CUTIN, A POLYESTER THAT
 FORMS THE STRUCTURE OF PLANT CUTICLE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- INDUCTION: AFTER CONTACT WITH CUTIN
 CC -1- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
 CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
 BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
 CC -1- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; K02640; AAA33334.1; -
 DR EMBL; M29759; AAA33335.1; -
 DR PIR; A00731; UVFUS.
 DR PIR; A32836; A32836.
 DR PDB; 1CUS; 31-JUL-94.
 DR PDB; 2CUT; 31-AUG-94.
 DR PDB; 1CUA; 11-JUL-96.
 DR PDB; 1CUB; 11-JUL-96.
 DR PDB; 1CUC; 11-JUL-96.
 DR PDB; 1CUD; 11-JUL-96.
 DR PDB; 1CUE; 11-JUL-96.
 DR PDB; 1CUF; 11-JUL-96.
 DR PDB; 1CUG; 11-JUL-96.
 DR PDB; 1CUH; 11-JUL-96.
 DR PDB; 1CUI; 11-JUL-96.
 DR PDB; 1CUJ; 11-JUL-96.
 DR PDB; 1CUU; 11-JUL-96.
 DR PDB; 1CUV; 11-JUL-96.
 DR PDB; 1CUW; 11-JUL-96.
 DR PDB; 1CUX; 11-JUL-96.
 DR PDB; 1CUI; 11-JUL-96.
 DR PDB; 1CUZ; 11-JUL-96.
 DR PDB; 1EFA; 08-MAR-96.
 DR PDB; 1EFB; 08-MAR-96.
 DR PDB; 1EFC; 08-MAR-96.
 DR PDB; 1EFD; 08-MAR-96.
 DR PDB; 1EFE; 08-MAR-96.
 DR PDB; 1CEX; 20-AUG-97.
 DR PDB; 1OXM; 15-MAY-97.
 DR PDB; 1XZA; 14-OCT-96.
 DR PDB; 1XZB; 14-OCT-96.
 DR PDB; 1XZC; 14-OCT-96.
 DR PDB; 1XZD; 14-OCT-96.
 DR PDB; 1XZE; 14-OCT-96.
 DR PDB; 1XZF; 14-OCT-96.
 DR PDB; 1XZG; 14-OCT-96.
 DR PDB; 1XZH; 14-OCT-96.
 DR PDB; 1XZI; 14-OCT-96.
 DR PDB; 1XZJ; 14-OCT-96.
 DR PDB; 1XZK; 30-NOV-96.
 DR PDB; 1XZL; 30-NOV-96.
 DR PDB; 1XZM; 30-NOV-96.
 DR PDB; 1AGY; 01-APR-98.
 DR GlycoSuiteDB; P00590; -
 DR InterPro; IPR000675; -
 DR Pfam; PF01083; Cutinase; 1.
 DR PRINTS; PR00129; CUTINASE.
 DR PROSITE; PS00155; CUTINASE_1; 1.
 DR PROSITE; PS00931; CUTINASE_2; 1.
 KW Hydrolase; Serine esterase; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 16
 FT CHAIN 17 230 CUTINASE.
 FT BINDING 32 32 GLUCURONIC ACID.
 FT DISULFID 47 194
 FT DISULFID 125 187

FT ACT_SITE 136 136
 FT ACT_SITE 191 191
 FT ACT_SITE 204 204
 FT CONFLICT 48 48 R -> A (IN REF. 2).
 FT CONFLICT 94 94 R -> A (IN REF. 2).
 SQ SEQUENCE 230 AA; 23982 MW; 7253ACAA657AD1AB CRC64;

Query Match 93.5%; Score 29; DB 1; Length 230;
 Best Local Similarity 85.7%; Pred. No. 5.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LASNLES 7
 Db 71 IASNLES 77

RESULT 9
 MYSS_CHICK STANDARD; PRT; 1938 AA.
 ID MYSS_CHICK AC P13538;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, ADULT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-205.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE=92041767; PubMed=1939027;
 RA Hayashida M., Maiba T., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: I.
 RL Sequence of the amino-terminal 23 kDa fragment.";
 RN J. Biochem. 110:54-59(1991).
 RN [2]
 RP SEQUENCE OF 206-636.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE=92041768; PubMed=1939028;
 RA Komine Y., Maiba T., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: II.
 RL Sequence of the 50 kDa fragment of subfragment-1.";
 RN J. Biochem. 110:60-67(1991).
 RN [3]
 RP SEQUENCE OF 637-837.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE=92041769; PubMed=1939029;
 RA Maiba T., Miyayoshi T., Matsuzono K., Tanioka Y., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: III.
 RL Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50
 RT kDa, and 22 kDa fragments.";
 RN J. Biochem. 110:68-74(1991).
 RN [4]
 RP SEQUENCE OF 838-1938.
 RC TISSUE=Pectoralis muscle;
 RX MEDLINE=92041770; PubMed=1939030;
 RA Maiba T., Yajima E., Nagata S., Miyayoshi T., Nakayama S., Matsuda G.;
 RT "The primary structure of skeletal muscle myosin heavy chain: IV.
 RL Sequence of the rod, and the complete 1,938-residue sequence of the
 RT heavy chain.";
 RN J. Biochem. 110:75-87(1991).
 RN [5]
 RP PRELIMINARY SEQUENCE OF 1-808.
 RX MEDLINE=87092420; PubMed=3467365;
 RA Maiba T., Hayashida M., Tanioka Y., Komine Y., Matsuda G.;
 RT "The primary structure of the myosin head.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:416-420(1987).
 RN [6]
 RP SEQUENCE OF 842-1270.
 RX MEDLINE=90121764; PubMed=2610940;

RA Watanabe B.;
 RT "Complete amino-acid sequence of subfragment-2 in adult chicken
 RL skeletal muscle myosin.";
 RL Biol. Chem. Hoppe-Seyler 370:1027-1034(1989).
 RN [7]
 RP SEQUENCE OF 852-1108.
 RX MEDLINE=89374803; PubMed=2775482;
 RA Watanabe B.;
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken
 RL skeletal muscle myosin.";
 RL Biol. Chem. Hoppe-Seyler 370:549-558(1989).
 RN [8]
 RP SEQUENCE OF 1145-1270
 RX MEDLINE=89228549; PubMed=2713098;
 RA Watanabe B.;
 RT "Amino-acid sequence of the hinge region in chicken myosin
 RL subfragment-2.";
 RL Biol. Chem. Hoppe-Seyler 370:55-61(1989).
 RN [9]
 RP SEQUENCE OF 1857-1938 FROM N.A.
 RX MEDLINE=87217964; PubMed=304534;
 RA Moriarty D.M., Barringer K.J., Dodgson J.B., Richter H.E.,
 RA Young R.B.;
 RT "Genomic clones encoding chicken myosin heavy-chain genes.";
 RL DNA 6:91-99(1987).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843.
 RX MEDLINE=93303624; PubMed=8316857;
 RA Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R.,
 RA Tomchick D.R., Benning M.M., Winkelman D.A., Wesenberg G.,
 RA Holden H.M.;
 RT "Three-dimensional structure of myosin subfragment-1: a molecular
 RL motor.";
 RL Science 261:50-58(1993).
 CC -I- FUNCTION: MUSCLE CONTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO
 CC F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
 CC -I- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -I- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
 CC -I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -I- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -I- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
 CC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
 CC CONSERVED.
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 CC -----
 CC EMBL: M16557; AAA48970.1;
 DR PIR: PX0050; PX0051.
 DR PIR: A26821; A26821.
 DR PIR: S02082; S02082.
 DR PIR: S04501; S04501.
 DR PIR: S05515; S05515.
 DR PDB: 2MYS; 11-JAN-97.
 DR InterPro: IPR000048;
 DR InterPro: IPR001609;
 DR InterPro: IPR002928;
 DR Pfam: PF00612; IQ: 1.
 DR Pfam: PF01576; Myosin_tail; 1.

RC STRAIN=ORSAY;
 RA Helig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + NICOTINAMIDE RIBONUCLEOTIDE =
 CC DIPHOSPHATE + NAD(+).
 CC -1- PATHWAY: NAD BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ARCHAEL NMN ADENYLTRANSFERASE
 CC FAMILY.
 CC
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 CC
 CC EMBL: AJ248288; CAB50478.1; -;
 CC InterPro: IPR001994; -;
 CC Pfam: PF01467; Cytidylyltransf; 1.
 CC Transferase: Nucleotidyltransferase; NAD.
 CC SEQUENCE 186 AA; 21417 MW; E8230B688481386E CRC64;

Query Match 90.3%; Score 28; DB 1; Length 186;
 Best Local Similarity 85.7%; Pred. No. 7.9;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 II:IIII
 Db 166 LATNLES 172

RESULT 12
 NADM_PYRHO STANDARD; PRT; 186 AA.
 AC O58211;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE NICOTINAMIDE-NUCLEOTIDE ADENYLTRANSFERASE (EC 2.7.7.1) (NAD(+)
 DE PYROPHOSPHORYLASE) (NAD(+)) DIPHOSPHORYLASE (NMN ADENYLTRANSFERASE).
 GN PH0464.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3.
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + NICOTINAMIDE RIBONUCLEOTIDE =
 CC DIPHOSPHATE + NAD(+).
 CC -1- PATHWAY: NAD BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ARCHAEL NMN ADENYLTRANSFERASE
 CC FAMILY.
 CC
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 CC
 CC EMBL: AP000002; BAA29550.1; -;
 CC InterPro: IPR001994; -;
 CC Pfam: PF01467; Cytidylyltransf; 1.
 CC Transferase: Nucleotidyltransferase; NAD.
 CC SEQUENCE 186 AA; 21392 MW; 1CE5A40C884ADB34 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 186;
 Best Local Similarity 85.7%; Pred. No. 7.9;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 II:IIII
 Db 166 LATNLES 172

RESULT 13
 YKY4_CAEEL STANDARD; PRT; 376 AA.
 AC Q17963;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL 40.4 KDA TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN
 DE CHROMOSOME III.
 DE C14B1.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Harris B.;

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: STRONG, TO K04G11.4 AND ZC302.2.

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 CC
 CC EMBL: Z37139; CAA85487.1; -;
 CC WormPep: C14B1.4; CE00901.
 CC InterPro: IPR001680; -;
 CC Pfam: PF00400; WD40; 7.
 CC PRINTS: PR00320; GPROTEINRPT
 CC PROSITE: PS00678; WD_REPEATS_1; 5.
 CC PROSITE: PS00682; WD_REPEATS_2; 6.
 CC PROSITE: PS0294; WD_REPEATS_REGION; 1.
 CC Hypothetical protein; Repeat; WD repeat.
 KW REPEAT 85 115 WD 1.
 FT REPEAT 127 157 WD 2.
 FT REPEAT 169 199 WD 3.
 FT REPEAT 211 241 WD 4.
 FT REPEAT 254 284 WD 5.
 FT REPEAT 296 329 WD 6.
 FT REPEAT 341 373 WD 7.
 SQ SEQUENCE 376 AA; 40393 MW; 3204DC36FE58FC19 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 376;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LASNLES 7
Db 272 LASNLS 278

RESULT 14
YN94_YEAST
ID YN94_YEAST STANDARD; PRT; 1116 AA.
AC P53751;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE PUTATIVE 125.2 KDA MEMBRANE GLYCOPROTEIN IN BIO3-HXT17 INTERGENIC
DE REGION.
GN YNR065C OR N3539.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PEPI FAMILY OF MEMBRANE GLYCOPROTEINS.
CC -----
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CC -----
DR EMBL; Z71680; CAA96347.1; -.
DR SGD; S0005348; YNR065C.
DR InterPro; IPR002860; -.
DR Pfam; PF02012; BNR; 7.
KW Hypothetical protein; Transmembrane; Glycoprotein.
FT TRANSMEM 934 957
FT CARBOHYD 35 35 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 846 846 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 985 985 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 1116 AA; 125199 MW; C0361878FE4DAB90 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 1116;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 534 LATNLES 540

RESULT 15
Y309_MYCGE
ID Y309_MYCGE STANDARD; PRT; 1225 AA.
AC P47551; O49317;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL LIPOPROTEIN MG309 PRECURSOR.
GN MG309.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AJCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;
RX Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 1138-1224 FROM N.A.
RC STRAIN-AJCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
CC ANCHOR (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; U39711; AAC71531.1; -.
DR EMBL; U02200; AAD12488.1; -.
DR TIGR; MG309; -.
KW Hypothetical protein; Lipoprotein; Membrane; Signal.
FT SIGNAL 1 27
FT CHAIN 28 1225 HYPOTHETICAL LIPOPROTEIN MG309.
FT LIPID 28 28 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 1185 1185 L -> V (IN REF. 2).
SQ SEQUENCE 1225 AA; 138375 MW; C3E4BF5B4319B6E8 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 1225;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
Db 286 LASNLS 292

Search completed: June 28, 2001, 15:54:39
Job time: 127 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:27 ; Search time 411.58 Seconds
(without alignments)
2.250 Million cell updates/sec

Title: US-09-724-406-30
Perfect score: 31
Sequence: 1 LASNLES 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_16:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	443	Q9LI76	Q9LI76 arabidopsis
2	31	100.0	826	Q9YHD5	Q9YHD5 rana catesb
3	29	93.5	856	Q9V706	Q9V706 drosophila
4	29	93.5	1939	Q13228	Q13228 gallus gall
5	29	93.5	1939	Q3PTT2	Q3PTT2 gallus gall
6	29	93.5	1941	Q9DGM4	Q9DGM4 gallus gall
7	29	93.5	1944	Q9DGM5	Q9DGM5 gallus gall
8	28	90.3	367	Q22481	Q22481 caenorhabdi
9	28	90.3	393	Q9X5A4	Q9X5A4 treponema d
10	28	90.3	459	Q82521	Q82521 capsicum ch
11	28	90.3	708	Q9YHD7	Q9YHD7 rana catesb
12	28	90.3	879	Q9YHD8	Q9YHD8 rana catesb
13	28	90.3	990	Q9FHH2	Q9FHH2 arabidopsis
14	27	87.1	125	Q95054	Q95054 trichomonas
15	27	87.1	125	Q95055	Q95055 trichomonas
16	27	87.1	190	Q05621	Q05621 thioacillu
17	27	87.1	204	Q9U2Y4	Q9U2Y4 caenorhabdi
18	27	87.1	309	Q15785	Q15785 homo sapien
19	27	87.1	309	Q9NT23	Q9NT23 homo sapien

20	87.1	389	10	Q9SAF7	Q9saf7 arabidopsis
21	87.1	457	2	Q9PQY2	Q9pqy2 ureaplasma
22	87.1	486	10	Q9SR09	Q9sr09 arabidopsis
23	87.1	643	10	Q9LSX2	Q9lsx2 arabidopsis
24	87.1	789	2	Q9KLN8	Q9kin8 vibrio chol
25	87.1	942	3	O42938	O42938 schizosacch
26	87.1	1184	11	O54807	O54807 mus musculu
27	87.1	1195	13	Q9PUM2	Q9pum2 xenopus lae
28	87.1	1208	4	O75162	O75162 homo sapien
29	87.1	1335	10	Q9FNF5	Q9fnf5 arabidopsis
30	87.1	1661	5	Q27095	Q27095 trichomonas
31	87.1	2098	5	Q25757	Q25757 plasmodium
32	87.1	2114	5	O97267	O97267 plasmodium
33	83.9	123	1	O58242	O58242 pyrococcus
34	83.9	136	2	O56707	O56707 vibrio para
35	83.9	158	10	Q9FMG6	Q9fmg6 arabidopsis
36	83.9	190	2	O52004	O52004 streptococc
37	83.9	207	2	O51353	O51353 pseudomonas
38	83.9	247	2	Q9HKN8	Q9hxn8 pseudomonas
39	83.9	268	10	Q9ZW20	Q9zw20 arabidopsis
40	83.9	268	10	Q9ZW03	Q9zw03 arabidopsis
41	83.9	269	10	Q9ZW18	Q9zw18 arabidopsis
42	83.9	271	10	Q9ZW19	Q9zw19 arabidopsis
43	83.9	282	3	Q9UTQ5	Q9utq5 schizosacch
44	83.9	301	10	Q9SP04	Q9sp04 arabidopsis
45	83.9	355	5	Q9GNS8	Q9gns8 tritrichomo

* ALIGNMENTS

RESULT 1					
Q9LI76					
ID	Q9LI76	PRELIMINARY;	PRT;	443 AA.	
AC	Q9LI76;				
DT	01-OCT-2000 (Tremblrel. 15, Created)				
DT	01-OCT-2000 (Tremblrel. 15, Last annotation update)				
DT	01-MAR-2001 (Tremblrel. 15, Last annotation update)				
DE	SIMILARITY TO ELICITOR-INDUCIBLE RECEPTOR EIR.				
OS	Arabidopsis thaliana (Mouse-ear cross).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;				
OC	Brassicales; Brassicaceae; Arabidopsi				
OX	NCBI_taxid=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=COLUMBIA;				
RA	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=COLUMBIA;				
RX	PubMed=10907853;				
RA	Nakamura Y.;				
RT	"Structural analysis of Arabidopsis thaliana chromosome 3. II.				
RT	Sequence features of the regions of 4,251,695 bp covered by ninety pl,				
RT	TAC and BAC clones.,"				
RL	DNA Res. 7:217-221(2000).				
DR	EMBL; AP001313; BAB03087.1;				
DR	InterPro; IPR001360;				
DR	InterPro; IPR001611;				
DR	InterPro; IPR003592;				
DR	Pfam; PF00560; LRR; 4.				
DR	PRINTS; PR00019; LEURICHRPT.				
DR	PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.				
DR	SMART; SM00370; LRR; 1.				
KW	Receptor.				
SQ	SEQUENCE 443 AA; 49318 MW; 1E2D37B3F9066F4C CRC64;				

Query Match 100.0%; Score 31; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7

Db 104 LASNLES 110

RESULT 2

Q9VHD5 PRELIMINARY; PRT; 826 AA.

AC Q9VHD5;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE MYOSIN HEAVY CHAIN (FRAGMENT).

GN MHC-4.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TAIL MUSCLE; HINDLIMB MUSCLE;

RA Hu H., Merrifield P., Atkinson B.G.;

RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of

RT Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles.";

RL Dev. Genet. 0:0-0(1999).

DR EMBL: AF097907; AAD13772.1; -.

DR InterPro: IPR000533; -.

DR InterPro: IPR002928; -.

DR Pfam: PF01576; Myosin_tail; 1.

DR PRINTS: PR00194; TROPOMYOSIN.

FT NON_TER 1

SQ SEQUENCE 826 AA; 95361 MW; 8F9E3B0579D0F483 CRC64;

Query Match

Best Local Similarity 100.0%; Score 31; DB 13; Length 826;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7

Db 122 LASNLES 128

RESULT 3

Q9V706 PRELIMINARY; PRT; 856 AA.

AC Q9V706;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE CGI3942 PROTEIN.

GN CGI3942.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Balcer R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Duran-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of *Drosophila melanogaster*.";

Science 287:2185-2195(2000).

DR EMBL: AE003815; AAF58260.1; -.

DR FlyBase: FBgn003922; CG13942.

DR InterPro: IPR002965; -.

DR PRINTS: PR01217; PRICHEXTENSIN.

SQ SEQUENCE 856 AA; 93777 MW; 3B6C3F80DFEA12B7 CRC64;

Query Match 93.5%; Score 29; DB 5; Length 856;

Best Local Similarity 85.7%; Pred. No. 1.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7

Db 845 IASNLES 851

RESULT 4

O13228 PRELIMINARY; PRT; 1939 AA.

AC O13228;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE MYOSIN HEAVY CHAIN.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WHITE LEHORN; TISSUE=PECTORALIS MUSCLE;

RA Chao T.H., Bandman E., Moore L.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: U87231; AAB47555.1; -.

DR HSSP: P08799; IMMD.

DR InterPro: IPR000048; -.

DR InterPro: IPR001609; -.

DR InterPro: IPR002928; -.

DR Pfam: PF00063; myosin_head; 1.

DR Pfam: PF00612; IQ; 1.

DR Pfam: PF01576; Myosin_tail; 1.

DR PRINTS: PR00193; MYOSINHEAVY.

DR ProDom: PD000355; -; 1.

DR SMART: SM00015; IQ; 1.

SQ SEQUENCE 1939 AA; 223178 MW; 4D4E3E037B7550E9 CRC64;

Query Match 93.5%; Score 29; DB 13; Length 1939;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 ||||:||
 Db 1234 LASNMES 1240

RESULT 5
 Q9PTY2 PRELIMINARY; PRT; 1939 AA.
 AC Q9PTY2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SKELETAL MYOSIN HEAVY CHAIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Machida S., Matsuoaka R., Noda S., Hiratsuka E., Takagaki Y., Oana S.,
 Furutani Y., Nakajima H., Takao A., Momma K.;
 RT "Evidence for the expression of neonatal skeletal myosin heavy chain
 in primary myocardium and cardiac conduction tissue in the developing
 chick heart."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021180; BAA89233.1; -;
 DR HSP; P08799; ILVA.
 DR InterPro: IPR000048; -;
 DR InterPro: IPR000533; -;
 DR InterPro: IPR001609; -;
 DR InterPro: IPR002928; -;
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR SMART; SM00242; MYSC; 1.
 SQ SEQUENCE 1939 AA; 22940 MW; 0AAC40D61A2D07F3 CRC64;

Query Match 93.5%; Score 29; DB 13; Length 1939;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 ||||:||
 Db 1235 LASNMES 1241

RESULT 6
 Q9DGM4 PRELIMINARY; PRT; 1941 AA.
 AC Q9DGM4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE FAST MYOSIN HEAVY CHAIN ISOFORM 3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Q., Bandman E.;

RT "Seven skeletal myosin heavy chain genes (MyHC) are organized as a
 multigene complex in the chicken genome."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF272034; AAF99314.1; -;
 SQ SEQUENCE 1941 AA; 223162 MW; 9C8597C1CCCF1DEEC CRC64;

Query Match 93.5%; Score 29; DB 13; Length 1941;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 ||||:||
 Db 1236 LASNMES 1242

RESULT 7
 Q9DGM5 PRELIMINARY; PRT; 1944 AA.
 AC Q9DGM5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE FAST MYOSIN HEAVY CHAIN ISOFORM 2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Q., Bandman E.;
 RT "Seven skeletal myosin heavy chain genes (MyHC) are organized as a
 multigene complex in the chicken genome."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF272033; AAF99314.1; -;
 SQ SEQUENCE 1944 AA; 223211 MW; 154F438220072D68 CRC64;

Query Match 93.5%; Score 29; DB 13; Length 1944;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 ||||:||
 Db 1239 LASNMES 1245

RESULT 8
 Q22481 PRELIMINARY; PRT; 367 AA.
 AC Q22481;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE SIMILARITY TO C. ELEGANS HYPOPHETICAL PROTEIN.
 GN T1484.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Willson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.;

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Favello T.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50191; AAA91241.1; -;
 DR InterPro; IPR003406; -;
 DR Pfam; PF02485; Branch; 1.
 SQ SEQUENCE 367 AA; 43010 MW; 72CB4A155DD447D4 CRC64;

Query Match 90.3%; Score 28; DB 5; Length 367;
 Best Local Similarity 85.7%; Pred. No. 88;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 76 LSSNLES 82

RESULT 9
 Q9X5A4 PRELIMINARY; PRT; 393 AA.
 AC Q9X5A4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE FLAGELLAR SWITCH PROTEIN FLY.
 GN FLY.
 OS Treponema denticola.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=158;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35405;
 RA Stamm L.V., Bergen H.L.;
 RT "Sequences of the tap1, flgD, flgE, orf4, motA, motB, flilL, flilM,
 RT flilY, and flilP Treponema denticola genes.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF122909; AAD20623.1; -;
 DR InterPro; IPR001172; -;
 DR InterPro; IPR001543; -;
 DR Pfam; PF01052; Spore; 1.
 DR PRINTS; PR00956; FLGMOTORFLIN.
 KW Flagella.
 SQ SEQUENCE 393 AA; 41701 MW; EF9B924DCC2AA342 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 393;
 Best Local Similarity 85.7%; Pred. No. 94;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 54 LSSNLES 60

RESULT 10
 O82521 PRELIMINARY; PRT; 459 AA.
 AC O82521;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE PUTATIVE AMINOTRANSFERASE.
 OS Capsicum chinense.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; I;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;

OC Solanales; Solanaceae; Capsicum.
 OX NCBI_TaxID=80379;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HABANERO;
 RA Aluru M., Curry J., O'Connell M.A.;
 RT "Nucleotide sequence of a probable aminotransferase from habanero
 RT chile.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF095149; AAC78480.1; -;
 DR HSPF; P04181; 20AT.
 DR InterPro; IPR000954; -;
 DR Pfam; PF00202; aminotran_3; 1.
 DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN_1.
 KW Transferase; Aminotransferase.
 SQ SEQUENCE 459 AA; 50729 MW; 02ABB4D728B524E4 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 459;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 200 LANNLES 206

RESULT 11
 Q9YHD7 PRELIMINARY; PRT; 708 AA.
 AC Q9YHD7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).
 GN MHC-2.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TAIL MUSCLE, HINDLIMB MUSCLE;
 RA Hu H., Merrifield P., Atkinson B.G.;
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
 RT Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles.";
 RL Dev. Genet. 0:0-0(1999).
 DR EMBL; AF097905; AAD13770.1; -;
 DR InterPro; IPR000533; -;
 DR InterPro; IPR002928; -;
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 FT NON_TER
 SQ SEQUENCE 708 AA; 81823 MW; BE2D01700017BC4C CRC64;

Query Match 90.3%; Score 28; DB 13; Length 708;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 4 LASNLEN 10

RESULT 12
 Q9YHD8 PRELIMINARY; PRT; 879 AA.
 AC Q9YHD8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT).

GN MHC-1.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TAIL MUSCLE, HINDLIMB MUSCLE;
 RA Hu H., Merrifield P., Atkinson B.G.;
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of
 RT Thyroid Hormone-Induced Metamorphosing Rana catesbeiana Tadpoles.";
 RL Dev. Genet. 0:0-0(1999).
 DR EMBL; AF097904; AAD13769.1; -.
 DR InterPro; IPR000533; -.
 DR IPR002928; -.
 DR PFAM; PF01576; MYOSIN_TAIL; 1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 FT NON_TER 1
 SQ SEQUENCE 879 AA; 101710 MW; 1C456851E968A3D8 CRC64;

Query Match 90.3%; Score 28; DB 13; Length 879;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 Db 171 LASNLEN 177

RESULT 13
 Q9FHH2 PRELIMINARY; PRT; 990 AA.
 AC Q9FHH2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 101 KDA HEAT SHOCK PROTEIN, HSP101-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT P1 and TAC clones.";
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AB018118; BAB09589.1; -.
 KW Heat shock.
 SQ SEQUENCE 990 AA; 108709 MW; A0BA396F566466CB CRC64;

Query Match 90.3%; Score 28; DB 10; Length 990;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASNLES 7
 ||:||||
 Db 395 LANNLES 401

RESULT 14
 Q95054 PRELIMINARY; PRT; 125 AA.
 AC Q95054;
 ID Q95054;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE IRON SUPEROXIDE DISMUTASE (EC 1.15.1.1) (FRAGMENT).
 GN SOD3.
 OS Trichomonas vaginalis.
 OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonas.
 OX NCBI_TaxID=5722;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30001;
 RA Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30001;
 RA Touzel J.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30001;
 RX MEDLINE=97047378; PubMed=8892298;
 RA Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
 RT "Phylogenetic implication of iron-containing superoxide dismutase
 RT genes from trichomonad species.";
 RL Mol. Biochem. Parasitol. 80:209-214(1996).
 CC -|- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -|- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -|- COFACTOR: COPPER AND ZINC OR IRON OR MANGANESE.
 CC -|- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; Z70671; CAA94528.1; -.
 DR HSSP; P09157; IISC.
 DR InterPro; IPR001189; -.
 DR Pfam; PF00081; sodfe; 1.
 KW Oxidoreductase.
 FT NON_TER 1 125
 SQ SEQUENCE 125 AA; 13826 MW; 108A018B073F60DD CRC64;

Query Match 87.1%; Score 27; DB 5; Length 125;
 Best Local Similarity 85.7%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LASNLES 7
 |||||
 Db 64 LASNPES 70

RESULT 15
 Q95055 PRELIMINARY; PRT; 125 AA.
 AC Q95055;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE IRON SUPEROXIDE DISMUTASE (EC 1.15.1.1) (FRAGMENT).
 GN SOD3.
 OS Trichomonas vaginalis.
 OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonas.
 OX NCBI_TaxID=5722;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30001;
 RA Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 30001;
 RA Touzel J.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 30001;
 RX MEDLINE=97047378; PubMed=8892298;
 RA Viscogliosi E., Durieux I., Delgado-Viscogliosi P., Bayle D., Dive D.;
 RT "Phylogenetic implication of iron-containing superoxide dismutase
 genes from trichomonad species.";
 RL Mol. Biochem. Parasitol. 80:209-214(1996).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: COPPER AND ZINC OR IRON OR MANGANESE.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; 270672; CAA94529.1; -;
 DR HSP; P09157; IISC.
 DR InterPro; IPR001189; -;
 DR Pfam; PF00081; sodfe; 1.
 KW Oxidoreductase.
 FT NON_TER 1 1
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA; 13776 MW; 12CCEBCB433B80DD CRC64;

Query Match 87.1%; Score 27; DB 5; Length 125;
 Best Local Similarity 85.7%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LASNLES 7
 Db 64 LASNFES 70

Search completed: June 28, 2001, 16:08:27
 Job time: 955 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:14:39 ; Search time 362.28 Seconds
(without alignments)
1.506 Million cell updates/sec

Title: US-09-724-406-32
Perfect score: 50
Sequence: 1 QHSGELPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
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12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
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15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
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20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	84.0	111	17	AA1985242 Humanised antibody
2	42	84.0	111	17	AA1985236 Murine 206 antibod
3	40	80.0	9	16	AA195480 Mouse antibody lig
4	40	80.0	125	12	AA195440 Light chain variab
5	40	80.0	132	17	AA195440 Anti-human gp39 MA
6	39	78.0	405	21	AA195441 Human ORFX ORF2205
7	37	74.0	9	16	AA195475 Mouse antibody lig
8	37	74.0	21	15	AA195176 GM-CSF receptor al
9	37	74.0	111	13	AA195721 Humanised VL regio
10	37	74.0	111	22	AA195661 Murine Rd79 antibo
11	37	74.0	111	22	AA195662 Humanised Rd79 ant

12	37	74.0	218	16	AA195457 Mouse antibody FB3
13	37	74.0	218	16	AA195459 Mouse antibody F4-
14	36	72.0	9	21	AA195459 H. pylori HSP60-bi
15	36	72.0	111	15	AA195459 Light chain variab
16	36	72.0	111	21	AA195459 H. pylori HSP60-bi
17	36	72.0	212	15	AA195459 Porphyrin antibody
18	36	72.0	249	21	AA195459 Human prostate can
19	36	72.0	523	21	AA195459 Zebrafish PTH3R re
20	36	72.0	640	20	AA195459 Human CHD1 protein
21	36	72.0	648	20	AA195459 Human CHD1 protein
22	35	70.0	307	21	AA195459 Amino acid sequenc
23	35	70.0	307	21	AA195459 DNA encoding a pol
24	35	70.0	312	21	AA195459 Human ORFX ORF49
25	35	70.0	539	21	AA195459 Human nucleic acid
26	35	70.0	782	21	AA195459 Human ORFX ORF1983
27	34	68.0	56	19	AA195459 Ikaros protein SEQ
28	34	68.0	56	19	AA195459 Ikaros protein SEQ
29	34	68.0	84	21	AA195459 Ikaros protein SEQ
30	34	68.0	84	21	AA195459 PRDI-BF1 protein z
31	34	68.0	93	16	AA195459 Anti-HCV antibody
32	34	68.0	112	21	AA195459 Human secreted pro
33	34	68.0	136	21	AA195459 Human secreted pro
34	34	68.0	137	21	AA195459 Human secreted pro
35	34	68.0	179	21	AA195459 Gene 8 human secre
36	34	68.0	197	21	AA195459 Human ORFX ORF2394
37	34	68.0	197	21	AA195459 Human cell cycle r
38	34	68.0	219	21	AA195459 Human cancer assoc
39	34	68.0	252	17	AA195459 Human REST protein
40	34	68.0	308	17	AA195459 Human REST protein
41	34	68.0	318	21	AA195459 Amino acid sequenc
42	34	68.0	318	21	AA195459 Amino acid sequenc
43	34	68.0	334	17	AA195459 Ikaros protein. N
44	34	68.0	334	19	AA195459 Ikaros isoform. U
45	34	68.0	334	19	AA195459 Human Ikaros prote

ALIGNMENTS

RESULT 1

AA195457 standard; Protein; 111 AA.
AA195457;
09-APR-1996 (first entry)
Humanised antibody variable light chain region (VZV HuV).
Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
infection; detection; isolation; monoclonal antibody; MAb; mimetic;
humanised; murine; heavy chain; light chain; variable region; CDR;
NEW; REI.
Synthetic.
WO9531546-A1.
23-NOV-1995.
28-APR-1995; 95WO-US05305.
28-APR-1994; 94US-0234133.
(SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
Carr FJ, Harris WJ, Moss MT, Wallace TP;
WPI; 1996-010932/01.
Varicella zoster virus gpIII antibody with humanised variable region
- for treatment, prevention or diagnosis of varicella zoster virus
infections

XX Claim 7; Page 31; 58pp; English.
 PS
 CC Antibodies (Ab) comprising a humanised variable region specifically
 CC binding to a varicella zoster virus (VZV) can be used to treat or
 CC prevent VZV infection. They may optionally be attached to a
 CC therapeutic agent. They may also be used, when labelled, to detect
 CC VZV particles and infected cells in blood; for the removal/
 CC neutralisation of infectious VZV in blood; for the selection/
 CC isolation of human monoclonal Abs and for the design of (non-)
 CC peptide mimetics with similar diagnostic and therapeutic uses. The
 CC variable region CDR portion is derived from murine Ab 206 and the
 CC heavy and light chain variable region frameworks are NEMW and REI
 CC respectively. The framework may include at least one mutation that
 CC improves binding specificity or affinity. The heavy and light chain
 CC variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY,
 CC -VHKVRS or -VHS) and VZVHuVK respectively.
 XX
 SQ Sequence 111 AA;

Query Match 84.0%; Score 42; DB 17; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.29;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 Db 93 qhsrelpft 101

RESULT 2
 AAR85236
 ID AAR85236 standard; Protein; 111 AA.
 XX
 AC AAR85236;

XX 05-APR-1996 (first entry)
 XX
 DE Murine 206 antibody variable light chain region.

XX Antibody; varicella zoster virus; Ab; VSV; treatment; prevention;
 KW infection; detection; isolation; monoclonal antibody; MAB; mimetic;
 KW humanised; murine; heavy chain; light chain; variable region; CDR;
 KW NEMW; REI.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
 FH Binding-site 24..38
 FT /label= CDR 1.
 FT Binding-site 54..60
 FT /label= CDR 2.
 FT Binding-site 93..101
 FT /label= CDR 3.

XX W09531546-A1.
 PN
 XX
 PD 23-NOV-1995.
 XX
 PF 28-APR-1995; 95WO-US05305.
 XX
 PR 28-APR-1994; 94US-0234133.
 XX

XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
 XX Carr FJ, Harris WJ, Moss MT, Wallace TP;
 PI
 XX WPI; 1996-010932/01.
 DR N-PSDB; AAT06051.
 DR

XX Varicella zoster virus gpIII antibody with humanised variable region
 PT - for treatment, prevention or diagnosis of varicella zoster virus
 PT infections

XX Claim 2; Figure 2; 58pp; English.
 PS
 CC Antibodies (Ab) comprising a humanised variable region specifically
 CC binding to a varicella zoster virus (VZV) can be used to treat or
 CC prevent VZV infection. They may optionally be attached to a
 CC therapeutic agent. They may also be used, when labelled, to detect
 CC VZV particles and infected cells in blood; for the removal/
 CC neutralisation of infectious VZV in blood; for the selection/
 CC isolation of human monoclonal Abs and for the design of (non-)
 CC peptide mimetics with similar diagnostic and therapeutic uses. The
 CC variable region CDR portion is derived from murine Ab 206 and the
 CC heavy and light chain variable region frameworks are NEMW and REI
 CC respectively. The framework may include at least one mutation that
 CC improves binding specificity or affinity. The heavy and light chain
 CC variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY,
 CC -VHKVRS or -VHS) and VZVHuVK respectively.
 XX
 SQ Sequence 111 AA;

Query Match 84.0%; Score 42; DB 17; Length 111;
 Best Local Similarity 88.9%; Pred. No. 0.29;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 Db 93 qhsrelpft 101

RESULT 3
 AAR75480
 ID AAR75480 standard; Peptide; 9 AA.
 XX
 AC AAR75480;

XX 07-FEB-1996 (first entry)
 XX
 DE Mouse antibody light chain variable region CDR3 peptide #11.

XX Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
 KW antibody; immunotolerance; animal; variegated display library; CDR;
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
 KW familial hypercholesterolaemia; binding affinity;
 KW complementarity determining region.

XX Synthetic.
 OS
 XX W09515982-A2.
 PN
 XX 15-JUN-1995.
 PD
 XX 08-DEC-1994; 94WO-US14106.
 PF
 XX 06-DEC-1994; 94US-0350400.
 PR
 XX 08-DEC-1993; 93US-0164022.
 PR

XX (GENZ) GENZYME CORP.
 PA
 XX Barsomian G, Copeland DP, Hillhouse D, Johnson T;
 PI
 XX WPI; 1995-224291/29.
 DR

XX Generating new antibodies specific for immunorecessive epitopes -
 PT by selection from variegated V gene library cloned from
 PT immuno:tolerance derived antibody repertoire, useful in diagnosis,
 PT purificn. and therapy, e.g. of cancer
 XX
 XX Claim 43; Page 92; 109pp; English.

XX Peptides AAR75462-92 are examples of complementarity determining regions
 CC (CDRs) used to generate antibodies against immunorecessive antigens.

CC The CDRs are derived from the heavy and light chain variable regions of
 CC the antibodies FB3-2 (AAQ92500-1), F4-7 (AAQ92502-3) and H3-3
 CC (AAQ92504-5). The peptides AAR75470-81 represent CDR3 from the light
 CC chain variable regions. The CDR sequences were isolated from a
 CC variegated display library (VDL) of variable regions derived from a
 CC repertoire of antibodies from an immunotolerised animal. The VDL is
 CC generated by PCR amplifying the variable regions from the antibody coding
 CC sequences using the primers AAQ74153-74. The constructed antibodies are
 CC generated against an immunorecessive antigen e.g. a cell surface marker
 CC on a foetal, cancer or stem cell, which can differentiate between variant
 CC or related forms of the antigen. The antibodies generated can be used in
 CC the diagnosis, e.g. detection of the immunorecessive antigen, or in
 CC therapy e.g. of cancer, Alzheimer's disease or familial
 CC hypercholesterolaemia. The method of production of the antibody allows
 CC rapid and sensitive isolation of antibodies that would be difficult to
 CC isolate by standard methods. The antibodies produced have greater
 CC binding affinity than those produced by combinatorial/hybridoma methods.
 XX
 SQ Sequence 9 AA;

Query Match 80.0%; Score 40; DB 16; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3.4e+05;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 IIII:III
 Db 1 qhsweipft 9

RESULT 4
 AAR15440
 ID AAR15440 standard; Protein; 125 AA.
 AC AAR15440;

XX 25-FEB-1992 (first entry)

XX Light chain variable region of MAB 2C2.

XX HRV; ICAM-1; antigen-binding fragment; inflammation;
 KW auto-immune disease.

XX Homo sapiens.

XX EP459577-A.

XX 04-DEC-1991.

XX 25-MAY-1991; 91EP-0201243.

XX 01-JUN-1990; 90US-0532001.

XX (MERI) MERCK & CO INC.

XX Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
 XX WPI; 1991-355850/49.

XX Microbially expressed portions of monoclonal antibody - can block
 PT attachment of rhinovirus ligands to inter-cellular adhesion
 PT molecule (ICAM-1)
 XX
 XX Claim 1; Page 20; 28pp; English.

XX This is one of six antibody fragments from MAB's specific for domain
 CC 1 of ICAM-1. The peptide fragments can be used to treat or prevent
 CC rhinovirus infection. See AAR15437-R15443.
 XX
 SQ Sequence 125 AA;

Query Match 80.0%; Score 40; DB 12; Length 125;

Best Local Similarity 77.8%; Pred. No. 0.85;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QHSGELPFT 9
 IIII:III
 Db 93 qhsweipft 101

RESULT 5

AAW03723

ID AAW03723 standard; Protein; 132 AA.

XX AAW03723;

XX 02-APR-1997 (first entry)

XX Anti-human gp39 MAB 39-1.7 light chain variable region.

XX Light chain; variable region; murine; mouse; anti-human; disease;
 KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.7; hybridoma;
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder;
 KW immune; autoimmune; allergic response; organ rejection; drug;
 KW graft versus host; cell imaging; tumour; targeted; delivery;
 KW targeted.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Peptide /label= sig_peptide

XX Peptide 21..132

XX Region /label= mat_peptide

XX Region 44..58

XX Region /note= "complementarity determining region 1"

XX Region /note= "complementarity determining region 2"

XX Region /note= "complementarity determining region 3"

XX WO9623071-A2.

XX 01-AUG-1996.

XX 26-JAN-1996; 96WO-US01119.

XX 26-JAN-1995; 95US-0379057.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;
 XX Harris LJ, Hollenbaugh D, Siadak AW;

XX WPI; 1996-362694/36.

XX N-PSDB; AAT35975.

XX Monoclonal antibodies specific for different epitope(s) on human
 PT gp39 - used for inhibiting B cell activation and for the diagnosis
 PT of various disorders, e.g. cancer, psoriasis etc..
 XX
 XX Claim 93; Fig 7A: 167pp; English.

XX The present sequence is the light chain variable region of the
 CC murine anti-human glycoprotein (gp) 39 monoclonal antibody (MAB)
 CC 39-1.7 (a member of the murine kappa II subfamily). The MAB was
 CC prep'd. by immunising a 6-8 week old BALB/c mouse with a gp39-CD8
 CC fusion protein, and 3 days later harvesting and fusing spleen and
 CC lymph cells to mouse melanoma cells, to produce an anti-human gp39
 CC MAB producing hybridoma. The MAB may be useful for diagnosing
 CC disease states, inhibiting B-cell activation and for treating
 CC immunological disorders, e.g. autoimmune disorders, allergic
 CC responses, organ rejection and graft versus host disease. It may
 CC also be used for imaging cells which express gp39 on their surface,
 CC e.g. tumour cells, and to target therapeutic agents to such cells.

CC The MAB inhibits the CD40/gp39 interaction, therefore limiting both
 CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.
 CC specific to these antigens. A typical compsn. for intramuscular
 CC injection pref. contains 50 mg of MAB in 1 ml of sterile buffered
 CC water.

SQ Sequence 132 AA;

Query Match 80.0%; Score 40; DB 17; Length 132;
 Best Local Similarity 77.8%; Pred. No. 0.91;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9

Db 113 qhsweipft 121

RESULT 6

AAB42441

ID AAB42441 standard; Protein; 405 AA.

AC AAB42441;

XX 08-FEB-2001 (first entry)

DE Human ORFX ORF2205 polypeptide sequence SEQ ID NO:4410.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

XX N-PSDB; AAC76650.

XX Novel nucleic acids and peptides derived from open reading frame x,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 3603-3604; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;

CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX protein in gene therapy
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus, lupus
 CC hyperextension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX SQ Sequence 405 AA;

Query Match 78.0%; Score 39; DB 21; Length 405;

Best Local Similarity 87.5%; Pred. No. 5.1;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 8

Db 227 qhsgekpft 234

RESULT 7

AAR75475

ID AAR75475 standard; Peptide; 9 AA.

XX AAR75475;

XX 07-FEB-1996 (first entry)

DE Mouse antibody light chain variable region CDR3 peptide #6.

XX Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
 KW antibody; immunotolerance; animal; variegated display library; CDR;
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
 KW familial hypercholesterolaemia; binding affinity;
 KW complementarity determining region.

XX Synthetic.

XX WO9515982-A2.

XX 15-JUN-1995.

XX 08-DEC-1994; 94WO-US14106.

XX 06-DEC-1994; 94US-0350400.

XX 08-DEC-1993; 93US-0164022.

XX (GENZ) GENZYME CORP.

XX Barsomian G, Copeland DP, Hillhouse D, Johnson T;

XX WPI; 1995-224291/29.

XX Generating new antibodies specific for immunorecessive epitopes -
 PT by selection from variegated V gene library cloned from
 PT immunotolerance derived antibody repertoire, useful in diagnosis,
 PT purifon. and therapy, e.g. of cancer

XX Claim 43; Page 92; 109pp; English.

XX Peptides AAR75462-92 are examples of complementarity determining regions
 CC (CDRs) used to generate antibodies against immunorecessive antigens.

CC The CDRs are derived from the heavy and light chain variable regions of
 CC the antibodies FB3-2 (AA092500-1), F4-7 (AA092502-3) and H3-3
 CC (AA092504-5). The peptides AAR75470-81 represent CDR3 from the light
 CC chain variable regions. The CDR sequences were isolated from a
 CC variegated display library (VDL) of variable regions derived from a
 CC repertoire of antibodies from an immunotolerised animal. The VDL is
 CC generated by PCR amplifying the variable regions from the antibody coding
 CC sequences using the primers AA074153-74. The constructed antibodies are
 CC generated against an immunorecessive antigen e.g. a cell surface marker
 CC on a foetal cancer or stem cell, which can differentiate between variant
 CC or related forms of the antigen. The antibodies generated can be used in
 CC the diagnosis, e.g. detection of the immunorecessive antigen, or in
 CC therapy e.g. of cancer, Alzheimer's disease or familial
 CC hypercholesterolaemia. The method of production of the antibody allows
 CC rapid and sensitive isolation of antibodies that would be difficult to
 CC isolate by standard methods. The antibodies produced have greater
 CC binding affinity than those produced by combinatorial/hybridoma methods.

XX SQ Sequence 9 AA;

Query Match 74.0%; Score 37; DB 16; Length 9;
 Best Local Similarity 66.7%; Pred. No. 3.4e+05;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 DB 1 qhsweipyt 9

RESULT 8
 AAR85176
 ID AAR85176 standard; peptide; 21 AA.

AC AAR85176;

DT 06-JUN-1996 (first entry)

DE GM-CSF receptor alpha-chain binding peptide.

XX Alpha-chain; GM-CSF; receptor; granulocyte; macrophage;
 KW colony stimulating factor; binding assay; antagonist;
 KW inflammation; autoimmune disease; agonist; upregulator;
 KW immune system cell; CDR III; light chain; antibody 23.2.

XX Synthetic.

XX W09529690-A1.

XX 09-NOV-1995.

XX 26-APR-1995; 95WO-US05160.

XX 29-APR-1994; 94US-0235404.

XX (UYPE-) UNIV PENNSYLVANIA.

XX (WIST-) WISTAR INST.

PI Kleber-Emmons T, Von Feldt JM, Weiner DB, Williams WV;

XX WPI; 1995-392919/50.

XX Identifying biologically active protein peptide mimics - by prepn.
 PT of recombinant antibody libraries and synthesising complementary
 PT determining region sequences.

XX Claim 13; Page 49; 70pp; English.

XX The present peptide binds the alpha-chain of the GM-CSF receptor,
 CC and can therefore be used in binding assays in place of GM-CSF. It
 CC can also be used as an antagonist, i.e. in the treatment of
 CC inflammation or autoimmune diseases, or in the prodn. of GM-CSF
 CC agonists, i.e. upregulators for the prodn. of immune system cells.

CC The peptide is derived from CDR III of the recombinant antibody
 CC light chain analogue of GM-CSF, 23.2.

XX SQ Sequence 21 AA;

Query Match 74.0%; Score 37; DB 16; Length 21;
 Best Local Similarity 77.8%; Pred. No. 0.5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 DB 2 qhsrelpwt 10

RESULT 9

AAR25721
 ID AAR25721 standard; Protein; 111 AA.

AC AAR25721;

DT 13-JAN-1993 (first entry)

DE Humanised VL region of the mouse Fd79 antibody.

XX Murine; immunoglobulin; CDR; HSV; non immunogenic; herpes simplex
 KW virus; HSV; light chain; variable region; framework; human; Pom.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 24..38

FT /note= "CDR"

FT Region 54..60

FT /note= "CDR"

FT Region 93..100

FT /note= "CDR"

FT Misc-difference 9

FT /note= "mutated residue"

FT Misc-difference 45

FT /note= "mutated residue"

FT Misc-difference 46

FT /note= "mutated residue"

FT Misc-difference 53

FT /note= "mutated residue"

FT Misc-difference 81

FT /note= "mutated residue"

FT Misc-difference 83

FT /note= "mutated residue"

XX W09211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coeligh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions

XX Claim 19; Fig 143; 141pp; English.

XX The sequence shows the humanised mature light chain variable
 CC region of the mouse Fd79 antibody. Murine CDRs were used in a

CC human Pom framework to produce a pure humanised immunoglobulin (Ig)
 CC which is capable of binding to a herpes simplex virus-specific
 CC epitope. The Ig is non immunogenic, due to the human framework,
 CC and has a strong affinity for its predetermined antigen. They can
 CC be produced in large quantities via recombinant DNA and monoclonal
 CC antibody technology. The humanised Igs may be used alone or in
 CC combination with chemotherapeutic agents such as non-steroidal
 CC anti-inflammatory drugs or immunosuppressants.
 CC See also AAR25722-32.

XX SQ Sequence 111 AA;

Query Match 74.0%; Score 37; DB 13; Length 111;
 Best Local Similarity 66.7%; Pred. No. 3.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 ||| |::|
 Db 93 qhsweipyt 101

RESULT 10
 AAB69661
 ID AAB69661 standard; Protein; 111 AA.

XX AC AAB69661;

XX 30-APR-2001 (first entry)

XX Murine Fd79 antibody light chain SEQ ID NO: 46.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

XX US6180370-BL.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 PS Example 6; Fig 2; 145pp; English.

XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

SQ Sequence 111 AA;

Query Match 74.0%; Score 37; DB 22; Length 111;
 Best Local Similarity 66.7%; Pred. No. 3.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 ||| |::|
 Db 93 qhsweipyt 101

RESULT 11

AAB69662

ID AAB69662 standard; Protein; 111 AA.

XX AC AAB69662;

XX 30-APR-2001 (first entry)

XX Humanised Fd79 antibody light chain SEQ ID NO: 47.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

XX Homo sapiens.

XX US6180370-BL.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell
 PT containing DNA segments encoding humanized heavy and light chain
 PT variable regions, and expressing the DNA segments in the cell -
 PS Example 6; Fig 2; 145pp; English.

XX The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

XX SQ Sequence 111 AA;

Query Match 74.0%; Score 37; DB 22; Length 111;
 Best Local Similarity 66.7%; Pred. No. 3.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 ||| |::|

Db 93 qhsweipyt 101

RESULT 12

AAR75457
ID AAR75457 standard; Protein; 218 AA.

XX AC AAR75457;
XX DT 07-FEB-1996 (first entry)

XX DE Mouse antibody FB3-2 light chain variable region protein sequence.
XX KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
XX KW antibody; immunotolerance; animal; variegated display library;
XX KW variable region; antigen; immunorecessive; cell surface marker; foetal;
XX KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
XX KW familial hypercholesterolaemia; binding affinity.

XX OS Mus musculus.

XX PN W09515982-A2.

XX PD 15-JUN-1995.

XX PF 08-DEC-1994; 94WO-US14106.

XX PR 06-DEC-1994; 94US-0350400.

XX PR 08-DEC-1993; 93US-0164022.

XX PA (GENZ) GENZYME CORP.

XX PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;

XX DR WPI; 1995-224291/29.

XX DR N-PSDB; AAQ92501.

XX PT Generating new antibodies specific for immunorecessive epitopes
XX PT by selection from variegated V gene library cloned from
XX PT immunotolerance derived antibody repertoire, useful in diagnosis,
XX PT purificn. and therapy, e.g. of cancer

XX PS Disclosure; Page 76-77; 109pp; English.

XX CC The sequence of the light chain variable region from the mouse antibody
XX CC FB3-2. This sequence was isolated from a variegated display library
XX CC (VDL) of variable regions derived from a repertoire of antibodies from
XX CC an immunotolerised animal. The VDL is generated by PCR amplifying the
XX CC variable regions from the antibody coding sequences using the primers
XX CC AAQ74153-74. The variable regions, esp the complementarity determining
XX CC regions (CDR; see AAR75462-93 for examples of CDRs) from the
XX CC immunotolerant animals' antibodies are used to construct an antibody
XX CC against a immunorecessive antigen e.g. a cell surface marker on a foetal,
XX CC cancer or stem cell, which can differentiate between variant or related
XX CC forms of the antigen. The antibodies generated can be used in the
XX CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
XX CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
XX CC The method of production of the antibody allows rapid and sensitive
XX CC isolation of antibodies that would be difficult to isolate by standard
XX CC methods. The antibodies produced have greater binding affinity than
XX CC those produced by combinatorial/hybridoma methods.

XX SQ Sequence 218 AA;

Query Match 74.0%; Score 37; DB 16; Length 218;

Best Local Similarity 66.7%; Pred. No. 6.6;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9

||| |::|

Db 93 qhsweipyt 101

RESULT 13

AAR75459

XX AC AAR75459 standard; Protein; 218 AA.

XX AC AAR75459;

XX DT 07-FEB-1996 (first entry)

XX DE Mouse antibody F4-7 light chain variable region protein sequence.
XX KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
XX KW antibody; immunotolerance; animal; variegated display library;
XX KW variable region; antigen; immunorecessive; cell surface marker; foetal;
XX KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
XX KW familial hypercholesterolaemia; binding affinity.

XX OS Mus musculus.

XX PN W09515982-A2.

XX PD 15-JUN-1995.

XX PF 08-DEC-1994; 94WO-US14106.

XX PR 06-DEC-1994; 94US-0350400.

XX PR 08-DEC-1993; 93US-0164022.

XX PA (GENZ) GENZYME CORP.

XX PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;

XX DR WPI; 1995-224291/29.

XX DR N-PSDB; AAQ92503.

XX PT Generating new antibodies specific for immunorecessive epitopes
XX PT by selection from variegated V gene library cloned from
XX PT immunotolerance derived antibody repertoire, useful in diagnosis,
XX PT purificn. and therapy, e.g. of cancer

XX PS Disclosure; Page 80-81; 109pp; English.

XX CC The sequence of the light chain variable region from the mouse antibody
XX CC F4-7. This sequence was isolated from a variegated display library (VDL)
XX CC of variable regions derived from a repertoire of antibodies from an
XX CC immunotolerised animal. The VDL is generated by PCR amplifying the
XX CC variable regions from the antibody coding sequences using the primers
XX CC AAQ74153-74. The variable regions, esp the complementarity determining
XX CC regions (CDR; see AAR75462-93 for examples of CDRs) from the
XX CC immunotolerant animals' antibodies are used to construct an antibody
XX CC against a immunorecessive antigen e.g. a cell surface marker on a foetal,
XX CC cancer or stem cell, which can differentiate between variant or related
XX CC forms of the antigen. The antibodies generated can be used in the
XX CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
XX CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
XX CC The method of production of the antibody allows rapid and sensitive
XX CC isolation of antibodies that would be difficult to isolate by standard
XX CC methods. The antibodies produced have greater binding affinity than
XX CC those produced by combinatorial/hybridoma methods.

XX SQ Sequence 218 AA;

Query Match 74.0%; Score 37; DB 16; Length 218;

Best Local Similarity 66.7%; Pred. No. 6.6;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9

||| |::|

Db 93 qhsweipyt 101

RESULT 14

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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:01:15 ; Search time 138.34 Seconds
(without alignments)
1.311 Million cell updates/sec

Title: US-09-724-406-32
Perfect score: 50
Sequence: 1 QHSGELPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	80.0	9	5	PCT-US94-14106-46
2	40	80.0	132	2	US-08-379-057-16
3	37	74.0	9	5	PCT-US94-14106-40
4	37	74.0	21	2	US-08-711-212-2
5	37	74.0	21	5	PCT-US95-05160-2
6	37	74.0	111	1	US-07-634-278-47
7	37	74.0	111	1	US-07-634-278-47
8	37	74.0	111	1	US-08-477-728-46
9	37	74.0	111	1	US-08-477-728-47
10	37	74.0	111	1	US-08-474-040-46
11	37	74.0	111	1	US-08-474-040-47
12	37	74.0	111	1	US-08-487-200-46
13	37	74.0	111	1	US-08-487-200-47
14	37	74.0	111	4	US-08-484-537-46
15	37	74.0	111	4	US-08-484-537-47
16	37	74.0	111	5	PCT-US94-14106-53
17	37	74.0	218	5	PCT-US94-14106-57
18	37	74.0	453	6	5206152-7
19	36	72.0	77	2	US-08-570-227A-6
20	36	72.0	77	4	US-09-077-991-8
21	36	72.0	111	1	US-08-207-169A-4
22	36	72.0	640	4	US-09-262-773-4
23	36	72.0	648	4	US-09-262-773-2
24	34	68.0	56	4	US-08-711-417C-186
25	34	68.0	56	4	US-08-711-417C-187
26	34	68.0	56	4	US-08-711-417C-188
27	34	68.0	56	4	US-08-711-417C-189

28	34	68.0	77	2	US-08-570-227A-4	Sequence 4, Appl
29	34	68.0	77	4	US-09-077-991-6	Sequence 6, Appl
30	34	68.0	84	2	US-08-459-568-62	Sequence 62, Appl
31	34	68.0	84	2	US-08-399-411-62	Sequence 62, Appl
32	34	68.0	84	3	US-08-516-859A-62	Sequence 62, Appl
33	34	68.0	93	1	US-08-083-947-12	Sequence 12, Appl
34	34	68.0	93	5	PCT-US94-07088-12	Sequence 12, Appl
35	34	68.0	334	4	US-08-711-417C-201	Sequence 201, App
36	34	68.0	338	2	US-08-933-750C-4	Sequence 4, Appl
37	34	68.0	338	4	US-09-234-613-4	Sequence 4, Appl
38	34	68.0	390	4	US-08-711-417C-199	Sequence 199, App
39	34	68.0	431	4	US-08-711-417C-195	Sequence 195, App
40	34	68.0	432	4	US-08-711-417C-197	Sequence 197, App
41	34	68.0	461	4	US-08-711-417C-196	Sequence 196, App
42	34	68.0	470	2	US-08-465-590-153	Sequence 153, App
43	34	68.0	470	4	US-08-283-300A-13	Sequence 13, Appl
44	34	68.0	470	4	US-08-711-417C-153	Sequence 153, App
45	34	68.0	470	5	PCT-US95-09345-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
PCT-US94-14106-46
; Sequence 46, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US94-14106-46

Query Match 80.0%; Score 40; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPPT 9
||| |
Db 1 QHSGELPPT 9

RESULT 2
US-08-379-057-16
; Sequence 16, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Gordon, Marcia L.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Aruffo, Alejandro A.
; TITLE OF INVENTION: Monoclonal Antibodies Specific For
; TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use
; TITLE OF INVENTION: In Diagnosis and Therapy
; NUMBER OF SEQUENCES: 57

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Bristol-Myers Squibb Company
;; STREET: 3005 First Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/379,057
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ON0133-
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 727-3670
;; TELEFAX: (206) 727-3601
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 132 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: N-terminal
US-08-379-057-16

Query Match 80.0%; Score 40; DB 2; Length 132;
Best Local Similarity 77.8%; Pred. No. 0.45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGLPFT 9
Db 113 QHSWEIPFT 121

RESULT 3
PCT-US94-14106-40
;; Sequence 40, Application PC/TUS9414106
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Process for Generating Specific Antibodies
;; NUMBER OF SEQUENCES: 61
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII (text)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/14106
;; FILING DATE:
;; CLASSIFICATION:
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
PCT-US94-14106-40

Query Match 74.0%; Score 37; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGLPFT 9

Db 1 QHSWEIPFT 9
RESULT 4
US-08-712-212-2
;; Sequence 2, Application US/08712212
;; Patent No. 5837460
;; GENERAL INFORMATION:
;; APPLICANT: Williams, William V.
;; APPLICANT: Kieber-Emmons, Thomas
;; APPLICANT: Weiner, David B.
;; APPLICANT: Vonfeldt, Joan M.
;; TITLE OF INVENTION: Biologically active peptides and
;; TITLE OF INVENTION: methods of identifying the same
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: No. 5837460ris
;; STREET: One Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/712,212
;; FILING DATE: 03-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/235,404
;; FILING DATE: 29-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: UPN-1554
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-712-212-2

Query Match 74.0%; Score 37; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGLPFT 9
Db 2 QHSRELPT 10

RESULT 5
PCT-US95-05160-2
;; Sequence 2, Application PC/TUS9505160
;; GENERAL INFORMATION:
;; APPLICANT: Williams, William V.
;; APPLICANT: Kieber-Emmons, Thomas
;; APPLICANT: Weiner, David B.
;; TITLE OF INVENTION: Biologically active peptides and
;; TITLE OF INVENTION: methods of identifying the same
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05160
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,404
FILING DATE: 29-APR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2245
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05160-2

Query Match 74.0%; Score 37; DB 5; Length 21;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 QHSGLPFT 9
Db 2 QHSRLPWT 10

RESULT 6
US-07-634-278-46
; Sequence 46, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-46

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGLPFT 9
Db 93 QHSWEIPYT 101

RESULT 7
US-07-634-278-47
; Sequence 47, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975

; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-634-278-47

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
Db 93 QHSWEIPYT 101

RESULT 8
US-08-477-728-46
; Sequence 46, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-728-46

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
Db 93 QHSWEIPYT 101

RESULT 9
US-08-477-728-47
; Sequence 47, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-728-47

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
||| |::|
Db 93 QHSWEIPYT 101

RESULT 10
US-08-474-040-46
; Sequence 46, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-46

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
||| |::|
Db 93 QHSWEIPYT 101

RESULT 11
US-08-474-040-47
; Sequence 47, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-47

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
||| |::|
Db 93 QHSWEIPYT 101

RESULT 12
US-08-487-200-46
; Sequence 46, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-46

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPFT 9
Db 93 QHSWEIPT 101

RESULT 13
US-08-487-200-47
Sequence 47, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-47

Query Match 74.0%; Score 37; DB 1; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPFT 9
Db 93 QHSWEIPT 101

RESULT 14
US-08-484-537-46
Sequence 46, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-46

Query Match 74.0%; Score 37; DB 4; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
Db 93 QHSWEIPYT 101

RESULT 15
US-08-484-537-47
Sequence 47, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-47

Query Match 74.0%; Score 37; DB 4; Length 111;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
Db 93 QHSWEIPYT 101

Search completed: June 28, 2001, 16:01:15
Job time: 523 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:58:46 ; Search time 234.85 Seconds
(without alignments)
2.919 Million cell updates/sec

Title: US-09-724-406-32
Perfect score: 50
Sequence: 1 QHSGELPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 7617452 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	80.0	102	2 PH1077	Ig light chain V r
2	39	78.0	223	2 S06576	finger protein (cl
3	39	78.0	405	2 T42663	hypothetical prote
4	39	78.0	594	2 T16387	hypothetical prote
5	37	74.0	101	2 S59640	Ig light chain V r
6	37	74.0	111	2 S09963	Ig kappa chain V-J
7	37	74.0	210	2 A56169	Ig kappa chain V r
8	37	74.0	384	2 I40867	hypothetical prote
9	37	74.0	1143	2 B84431	probable receptor
10	36	72.0	52	2 F43284	finger protein ZNF
11	36	72.0	111	1 KVM575	Ig kappa chain V r
12	36	72.0	111	1 KVM585	Ig kappa chain V r
13	36	72.0	112	2 S06562	finger protein (cl
14	36	72.0	138	2 S06571	finger protein (cl
15	36	72.0	140	2 S06574	finger protein (cl
16	36	72.0	157	2 S06532	finger protein (cl
17	36	72.0	169	2 S06580	finger protein (cl
18	36	72.0	196	2 S06558	finger protein (cl
19	36	72.0	196	2 S06581	finger protein (cl
20	36	72.0	196	2 S06561	finger protein (cl
21	36	72.0	196	2 S06555	finger protein (cl
22	36	72.0	214	2 S00832	finger protein (cl
23	36	72.0	218	2 S68241	Ig kappa chain V r
24	36	72.0	218	2 JC5810	monoclonal antibod
25	36	72.0	247	2 S06553	finger protein (cl
26	36	72.0	252	2 S06567	finger protein (cl
27	36	72.0	280	2 S06572	finger protein (cl
28	36	72.0	336	2 S06573	finger protein (cl
29	36	72.0	336	2 S06578	finger protein (cl

ALIGNMENTS

RESULT 1

PH1077

Ig light chain V region (clone 17s-c4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1077

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1077

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-102 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 0.62;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9

Db 93 QHSWEIPT 101

RESULT 2

S06576

finger protein (clone XlcGF52-1) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993

C:Accession: S06576

R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Kno

J. Mol. Biol. 208, 639-659, 1989

A:Title: Second-order repeats in Xenopus laevis finger proteins.

A:Reference number: S05632; MUID:90040698

A:Accession: S06576

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-223 <NIE>

C:Keywords: DNA binding; zinc finger

Query Match 78.0%; Score 39; DB 2; Length 223;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9

|||||

Db 195 HSGEKPF 202

RESULT 3

T42663

hypothetical protein DKFZp434N0615.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T42663

R:Boecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22230

A:Accession: T42663

A:Molecule type: mRNA

A:Residues: 1-405 <HAA>

A:Cross-references: EMBL:AL133062

A:Experimental source: adult testis; clone DKFZp434N0615

C:Genetics:

A:Note: DKFZp434N0615.1

Query Match 78.0%; Score 39; DB 2; Length 405;

Best Local Similarity 87.5%; Pred. No. 4.4;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 8

Db 227 QHSGEKPF 234

RESULT 4

T16387

hypothetical protein F47E1.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16387

R:Favell, T.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F47E1.

A:Reference number: Z18505

A:Accession: T16387

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-594 <FAV>

A:Cross-references: EMBL:U39993; NID:g1055098; PID:g1055099; PIDN:AAA81086.1; CESP:F47E1

C:Genetics:

A:Gene: CESP:F47E1.3

A:Introns: 20/1; 54/3; 78/3; 104/3; 163/3; 186/3; 297/2; 352/1; 396/3; 457/1; 502/2; 541

Query Match 78.0%; Score 39; DB 2; Length 594;

Best Local Similarity 87.5%; Pred. No. 6.7;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 8

Db 573 QHSGEKPF 580

RESULT 5

S59640

Ig light chain V region N10 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000

C:Accession: S59640

R:Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sherliff, S.

J. Mol. Biol. 253, 559-575, 1995

A:Title: The crystal structure of the antibody N10-staphylococcal nuclease complex at 2.

A:Reference number: S59639; MUID:96068846

A:Accession: S59640

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-101 <BOS>

A:Cross-references: EMBL:U25122

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

E:6-84/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 37; DB 2; Length 101;

Best Local Similarity 66.7%; Pred. No. 2.5;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 9

Db 83 QHSGEIPYT 91

RESULT 6

S09963

Ig kappa chain V-J region (103-7E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000

C:Accession: S09963

R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo

A:Reference number: S09955; MUID:90269328

A:Accession: S09963

A:Molecule type: mRNA

A:Residues: 1-111 <REI>

A:Cross-references: EMBL:X51851

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

E:16-94/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 37; DB 2; Length 111;

Best Local Similarity 66.7%; Pred. No. 2.8;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 9

Db 93 QHSGEIPYT 101

RESULT 7

A56169

Ig kappa chain V region (clone 23.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000

C:Accession: A56169

R:Monfardini, C.; Kieber-Emmons, T.; Vonfeldt, J.M.; O'Malley, B.; Rosenbaum, H.; God

J. Biol. Chem. 270, 6628-6638, 1995

A:Title: Recombinant antibodies in bioactive peptide design.

A:Reference number: A56169; MUID:95204454

A:Accession: A56169

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-210 <MON>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 74.0%; Score 37; DB 2; Length 210;

Best Local Similarity 77.8%; Pred. No. 5.5;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 9

Db 93 QHSGELPWT 101

RESULT 8

I40867

hypothetical protein 2 - Clostridium perfringens
 C:Species: Clostridium perfringens
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
 C:Accession: I40867
 R:Traving, C.; Schauer, R.; Roggentin, P.
 Glycoconj. J. 11, 141-151, 1994
 A:Title: Gene structure of the 'large' sialidase isoenzyme from Clostridium perfringens
 A:Reference number: I40865; MUID:95102306
 A:Accession: I40867
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-384 <RES>
 A:Cross-references: EMBL:X87369; NID:g853805; PIDN:CAA60797.1; PID:g853808

Query Match 74.0%; Score 37; DB 2; Length 384;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 : | | | | |
 Db 157 KHIGDLPT 165

RESULT 9
 B84431
 Probable receptor protein kinase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: B84431
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: B84420; MUID:20083487
 A:Accession: B84431
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1143 <STO>
 A:Cross-references: GB:AE002093; NID:g4406778; PIDN:AAD20088.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g01950
 A:Map position: 2

Query Match 74.0%; Score 37; DB 2; Length 1143;
 Best Local Similarity 77.8%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 : | | | | |
 Db 646 QLSGELPFT 654

RESULT 10
 F43284
 finger protein ZNF52 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
 C:Accession: F43284
 R:Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.
 Genomics 13, 999-1007, 1992
 A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile sit
 A:Reference number: A43284; MUID:92372070
 A:Accession: F43284
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-52 <LIC>
 A:Cross-references: GB:M88361; NID:g340459; PID:g553813
 A:Note: sequence extracted from NCB1 backbone (NCBIN:111644, NCBIP:111646)
 C:Keywords: zinc finger

Query Match 72.0%; Score 36; DB 2; Length 52;
 Best Local Similarity 75.0%; Pred. No. 1.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 : | | | | |
 Db 21 HSGELPFT 28

RESULT 11
 KVMS75
 Ig kappa chain V region (PC7175) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Mar-2000
 C:Accession: B01938; A01938
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: B01938
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 72.0%; Score 36; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 : | | | | |
 Db 93 QHSRELPLT 101

RESULT 12
 KVMS85
 Ig kappa chain V regions (PC2485, PC4039) - mouse (tentative sequence)
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 31-Mar-2000
 C:Accession: A01939
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
 Nature 276, 785-790, 1978
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A:Reference number: A93204; MUID:79073152
 A:Accession: A01939
 A:Molecule type: protein
 A:Residues: 1-111 <WEI>
 A:Note: the PC4285 and PC4039 sequences are identical
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-94/Domain: immunoglobulin homology <IMM>
 F:23-92/Disulfide bonds: #status predicted

Query Match 72.0%; Score 36; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 : | | | | |
 Db 93 QHSRELPLT 101

RESULT 13
 S06562

finger protein (clone XlCGF9-1) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
 C:Accession: S06562
 R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoechel, J. Mol. Biol. 208, 639-659, 1989
 A:Title: Second-order repeats in Xenopus laevis finger proteins.
 A:Reference number: S05632; MUID:90040698
 A:Accession: S06562
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-112 <NIE>
 C:Keywords: DNA binding; zinc finger

Query Match 72.0%; Score 36; DB 2; Length 112;
 Best Local Similarity 75.0%; Pred. No. 4.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | |
 Db 56 HTGKPKFT 63

RESULT 14

S06571
 finger protein (clone XlCGF4-2) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 10-Oct-1997
 C:Accession: S06571
 R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoechel, J. Mol. Biol. 208, 639-659, 1989
 A:Title: Second-order repeats in Xenopus laevis finger proteins.
 A:Reference number: S05632; MUID:90040698
 A:Accession: S06571
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-138 <NIE>
 C:Superfamily: LIM metal-binding repeat homology
 C:Keywords: DNA binding; zinc finger
 F:34-93/Domain: LIM metal-binding repeat homology <LIM4>

Query Match 72.0%; Score 36; DB 2; Length 138;
 Best Local Similarity 75.0%; Pred. No. 5.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | |
 Db 54 HTGKPKFT 61

RESULT 15

S06574
 finger protein (clone XlCGF9-1) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
 C:Accession: S06574
 R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoechel, J. Mol. Biol. 208, 639-659, 1989
 A:Title: Second-order repeats in Xenopus laevis finger proteins.
 A:Reference number: S05632; MUID:90040698
 A:Accession: S06574
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-140 <NIE>
 C:Keywords: DNA binding; zinc finger

Query Match 72.0%; Score 36; DB 2; Length 140;
 Best Local Similarity 75.0%; Pred. No. 5.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | |
 Db 28 HTGKPKFT 35

Search completed: June 28, 2001, 15:58:47
 Job time: 375 sec



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OM protein - protein search, using sw model

Run on: June 28, 2001, 15:54:39 ; Search time 105.36 Seconds
(without alignments)
2.926 Million cell updates/sec

Title: US-09-724-406-32
Perfect score: 50
Sequence: 1 QHSGELPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	78.0	223	1 ZG52_XENLA	P18727 xenopus lae
2	36	72.0	111	1 KV3S_MOUSE	P01671 mus musculus
3	36	72.0	111	1 KV3U_MOUSE	P01673 mus musculus
4	36	72.0	112	1 ZG9_XENLA	P18738 xenopus lae
5	36	72.0	138	1 ZG44_XENLA	P18721 xenopus lae
6	36	72.0	140	1 ZG49_XENLA	P18724 xenopus lae
7	36	72.0	157	1 Z02_XENLA	P18743 xenopus lae
8	36	72.0	169	1 ZG62_XENLA	P18731 xenopus lae
9	36	72.0	196	1 ZG3_XENLA	P18718 xenopus lae
10	36	72.0	196	1 ZG64_XENLA	P18732 xenopus lae
11	36	72.0	196	1 ZG8_XENLA	P18737 xenopus lae
12	36	72.0	214	1 Z026_XENLA	P18746 xenopus lae
13	36	72.0	214	1 Z010_XENLA	P18739 xenopus lae
14	36	72.0	247	1 Z020_XENLA	P18744 xenopus lae
15	36	72.0	252	1 ZG28_XENLA	P18716 xenopus lae
16	36	72.0	280	1 ZG46_XENLA	P18722 xenopus lae
17	36	72.0	336	1 ZG57_XENLA	P18729 xenopus lae
18	36	72.0	337	1 ZG26_XENLA	P18715 xenopus lae
19	36	72.0	349	1 NTRB_ECOLI	P08712 escherichia
20	36	72.0	349	1 NTRB_ECOLI	P08712 escherichia
21	36	72.0	439	1 NTRB_ECOLI	P08712 escherichia
22	36	72.0	445	1 ZG5_XENLA	P06218 klebsiella
23	36	72.0	453	1 Z06_XENLA	P18725 xenopus lae
24	36	72.0	474	1 Z141_HUMAN	P18747 xenopus lae
25	36	72.0	647	1 ZG48_XENLA	P18749 xenopus lae
26	36	72.0	648	1 Z022_HUMAN	O15928 homo sapien
27	36	72.0	675	1 ZG20_XENLA	P18723 xenopus lae
28	36	72.0	697	1 ZG20_XENLA	O95125 homo sapien
29	35	70.0	321	1 Y441_HUMAN	P18714 xenopus lae
30	35	70.0	406	1 ZF59_MOUSE	O43167 homo sapien
31	35	70.0	589	1 Z132_HUMAN	O13360 homo sapien
32	34	68.0	56	1 ZN26_HUMAN	P52743 mus musculus
33	34	68.0	108	1 KV3V_MOUSE	P17031 homo sapien
					P01674 mus musculus

34	34	68.0	417	1 Z232_HUMAN	O9uny5 homo sapien
35	34	68.0	471	1 VCP_AEDAE	P42560 aedes aegyp
36	34	68.0	488	1 ZF92_MOUSE	O62396 mus musculus
37	34	68.0	512	1 Z169_HUMAN	O14929 homo sapien
38	34	68.0	517	1 IKAR_MOUSE	O03267 mus musculus
39	34	68.0	518	1 IKAR_CHICK	O42410 gallus gall
40	34	68.0	519	1 IKAR_HUMAN	O13422 homo sapien
41	34	68.0	521	1 ZN35_HUMAN	P13682 homo sapien
42	34	68.0	522	1 IKAR_ONCMY	O13089 oncorhynch
43	34	68.0	526	1 HELI_HUMAN	O9uks7 homo sapien
44	34	68.0	526	1 HELI_MOUSE	P81183 mus musculus
45	34	68.0	537	1 Z029_XENLA	P18748 xenopus lae

ALIGNMENTS

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RESULT 1
ZG52_XENLA
ID ZG52_XENLA STANDARD; PRT; 223 AA.
AC P18727;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE GASTRULA ZINC FINGER PROTEIN XLCGF52.1 (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90040698; PubMed=2509712;
RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
RA Poetling A., Knoechel W.;
RT "Second-order repeats in Xenopus laevis finger proteins.";
RL J. Mol. Biol. 208:639-659(1989).
PIR: S06576; S06576.
DR HSSP; P25490; 12NM.
DR InterPro; IPR000822;
DR Pfam; PF000096; zf-C2H2; 8.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
KW Zinc_finger; Metal-binding; DNA-binding; Repeat.
FT NON_TER 1
FT ZN_FING 6 27 C2H2-TYPE.
FT ZN_FING 33 55 C2H2-TYPE.
FT ZN_FING 61 83 C2H2-TYPE.
FT ZN_FING 89 111 C2H2-TYPE.
FT ZN_FING 117 139 C2H2-TYPE.
FT ZN_FING 145 167 C2H2-TYPE.
FT ZN_FING 173 195 C2H2-TYPE.
FT ZN_FING 201 223 C2H2-TYPE.
FT NON_TER 223
SQ SEQUENCE 223 AA; 25549 MW; BFA977BB6701BA96 CRC64;

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Query Match 78.0%; Score 39; DB 1; Length 223;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 HSGELPFT 9
Db 195 HSGELPFT 202

RESULT 2
KV3S_MOUSE STANDARD; PRT; 111 AA.
ID KV3S_MOUSE
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION PC 7175.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: B01938; KVM575
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 DB 93 QHSREPLT 101

RESULT 3
 KV3U_MOUSE
 ID KV3U_MOUSE STANDARD; PRT; 111 AA.
 AC P01673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 2485/PC 4039.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 CC !- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
 DR PIR: A01939; KVM585.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38
 FT DOMAIN 39 53
 FT DOMAIN 54 60
 FT DOMAIN 61 92
 FT DOMAIN 93 101
 FT DOMAIN 102 111
 FT DISULFID 23 92
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11986 MW; BF38C59AA7858467 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 111;
 Best Local Similarity 77.8%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
 DB 93 QHSREPLT 101

RESULT 4
 ZG9_XENLA
 ID ZG9_XENLA STANDARD; PRT; 112 AA.
 AC P18738;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF9.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR: S06562; S06562.
 DR HSSP: P08047; ISP2.
 DR InterPro: IPR000822; -
 DR Pfam: PF00096; zf-C2H2; 4.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12975 MW; ECE657AF564C7662 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 112;
 Best Local Similarity 75.0%; Pred. No. 2.3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 DB 56 HTGEKPT 63

RESULT 5
 ZG44_XENLA
 ID ZG44_XENLA STANDARD; PRT; 138 AA.
 AC P18721;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF44.2 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";

RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06571; S06571.
 DR HSP; P08047; 1SP2.
 DR InterPro: IPR000822; -.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 5 27 C2H2-TYPE.
 FT ZN_FING 32 54 C2H2-TYPE.
 FT ZN_FING 60 82 C2H2-TYPE.
 FT ZN_FING 88 110 C2H2-TYPE.
 FT ZN_FING 116 138 C2H2-TYPE.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 16316 MW; 3FC025908EEF43AB CRC64;

Query Match 72.0%; Score 36; DB 1; Length 138;
 Best Local Similarity 75.0%; Pred. No. 2.8;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HSGELPPT 9
 Db 54 HTGKPT 61

RESULT 6
 ZG49_XENLA STANDARD; PRT; 140 AA.
 ID ZG49_XENLA
 AC P18724;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF49.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06574; S06574.
 DR HSP; P25490; 12NM.
 DR InterPro: IPR000822; -.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 16386 MW; EPA279A81583E277 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 140;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HSGELPPT 9
 Db 28 HTGKPT 35

RESULT 7
 ZG62_XENLA STANDARD; PRT; 157 AA.
 ID ZG62_XENLA
 AC P18743;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE OOCYTE ZINC FINGER PROTEIN XLCGF2 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S05632; S05632.
 DR HSP; P08047; 1SP2.
 DR InterPro: IPR000822; -.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 79 101 C2H2-TYPE.
 FT ZN_FING 107 129 C2H2-TYPE.
 FT ZN_FING 135 157 C2H2-TYPE.
 FT NON_TER 157 157
 SQ SEQUENCE 157 AA; 17953 MW; 5386C35255E9AA6 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 157;
 Best Local Similarity 75.0%; Pred. No. 3.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HSGELPPT 9
 Db 129 HTGKPT 135

RESULT 8
 ZG62_XENLA STANDARD; PRT; 169 AA.
 ID ZG62_XENLA
 AC P18731;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF62.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06580; S06580.
 DR HSP; P08047; 1SP2.
 DR InterPro: IPR000822; -.
 DR Pfam; PF00096; zf-C2H2; 6.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 6.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.

FT NON_TER 1 1 C2H2-TYPE.
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 113 90 C2H2-TYPE.
 FT ZN_FING 119 141 C2H2-TYPE.
 FT ZN_FING 147 169 C2H2-TYPE.
 FT NON_TER 169 169
 SQ SEQUENCE 169 AA; 94EB7CBA8B177297 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 169;
 Best Local Similarity 75.0%; Pred. No. 3.5;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | | |
 Db 84 HTGEKPT 91

RESULT 9
 ZG3_XENLA STANDARD; PRT; 196 AA.
 AC P18718;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF3.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetling A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06558; S06558.
 DR HSP; P25490; 12NM.
 DR InterPro; IPR000822; .
 DR Pfam; PF00096; zf-C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.

FT NON_TER 1 1 C2H2-TYPE.
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT NON_TER 196 196
 SQ SEQUENCE 196 AA; 22378 MW; B5735306E722FDC CRC64;

Query Match 72.0%; Score 36; DB 1; Length 196;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | | |
 Db 28 HTGEKPT 35

RESULT 10
 ZG64_XENLA STANDARD; PRT; 196 AA.
 AC P18732;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF64.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetling A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06581; S06581.
 DR HSP; P08047; 1SP2.
 DR InterPro; IPR000822; .
 DR Pfam; PF00096; zf-C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1 C2H2-TYPE.
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT NON_TER 196 196
 SQ SEQUENCE 196 AA; 23052 MW; 15B0E600C8FEF9A8 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 196;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 I:| | | | |
 Db 84 HTGEKPT 91

RESULT 11
 ZG8_XENLA STANDARD; PRT; 196 AA.
 ID ZG8_XENLA
 AC P18737;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF8.2DB (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetling A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06561; S06561.
 DR HSP; P25490; 12NM.
 DR InterPro; IPR000822; .
 DR Pfam; PF00096; zf-C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1 C2H2-TYPE.
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.

FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT NON_TER 196
 SQ SEQUENCE 196 AA; C65153F709EDE461 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 196;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 DB 84 HTGKPT 91

RESULT 12
 Z026_XENLA STANDARD; PRT; 196 AA.
 AC P18746;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE OOCYTE ZINC FINGER PROTEIN XLCOF26 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Niefeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR: S06555; S06555.
 DR HSP: P25490; IZNM.
 DR InterPro: IPR000822;
 DR Pfam: PF00096; zf-C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT ZN_FING 1 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT NON_TER 196
 SQ SEQUENCE 196 AA; 22659 MW; A4417A032257D595 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 196;
 Best Local Similarity 75.0%; Pred. No. 4.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 DB 84 HTGKPT 91

RESULT 13
 Z010_XENLA STANDARD; PRT; 214 AA.
 AC P18739;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE OOCYTE ZINC FINGER PROTEIN XLCOF10 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89005062; PubMed=3139407;
 RA Koester M., Pieler T., Poeting A., Knoechel W.;
 RT "The finger motif defines a multigene family represented in the
 RT maternal mRNA of Xenopus laevis oocytes.";
 RL EMBO J. 7:1735-1741(1988).
 DR PIR: S00832; S00832.
 DR HSP: P08047; ISP2.
 DR InterPro: IPR000822;
 DR Pfam: PF00096; zf-C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT ZN_FING 1 23 C2H2-TYPE.
 FT ZN_FING 29 51 C2H2-TYPE.
 FT ZN_FING 57 79 C2H2-TYPE.
 FT ZN_FING 85 107 C2H2-TYPE.
 FT ZN_FING 113 135 C2H2-TYPE.
 FT ZN_FING 141 163 C2H2-TYPE.
 FT ZN_FING 169 191 C2H2-TYPE.
 SQ SEQUENCE 214 AA; 24830 MW; DCEEE00EDED1A5F8 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 214;
 Best Local Similarity 75.0%; Pred. No. 4.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 DB 107 HTGKPT 114

RESULT 14
 Z020_XENLA STANDARD; PRT; 247 AA.
 AC P18744;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE OOCYTE ZINC FINGER PROTEIN XLCOF20 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90040698; PubMed=2509712;
 RA Niefeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poeting A., Knoechel W.;
 RT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR: S06553; S06553.
 DR HSP: P08047; ISP2.
 DR InterPro: IPR000822;
 DR Pfam: PF00096; zf-C2H2; 8.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 8.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT ZN_FING 1 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.

FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT ZN_FING 225 247 C2H2-TYPE.
 FT NON_TER 247 247
 SQ SEQUENCE 247 AA; 28276 MW; C76B7808F6BE09AD CRC64;

Query Match 72.0%; Score 36; DB 1; Length 247;
 Best Local Similarity 75.0%; Pred. No. 5.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 Db 112 HTGEKPFT 119

RESULT 15
 ZG28_XENLA STANDARD; PRT; 252 AA.
 AC P18716;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE GASTRULA ZINC FINGER PROTEIN XLCGF28.1 (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90040698; PubMed-2509712;
 RA Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
 RA Poetig A., Knoechel W.;
 FT "Second-order repeats in Xenopus laevis finger proteins.";
 RL J. Mol. Biol. 208:639-659(1989).
 DR PIR; S06567; S06567.
 DR HSPP; P08047; ISP2.
 DR InterPro; IPR000822;
 DR Pfam; PF00096; zf-C2H2; 9.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 9.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 9.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
 FT NON_TER 1 1
 FT ZN_FING 6 28 C2H2-TYPE.
 FT ZN_FING 34 56 C2H2-TYPE.
 FT ZN_FING 62 84 C2H2-TYPE.
 FT ZN_FING 90 112 C2H2-TYPE.
 FT ZN_FING 118 140 C2H2-TYPE.
 FT ZN_FING 146 168 C2H2-TYPE.
 FT ZN_FING 174 196 C2H2-TYPE.
 FT ZN_FING 202 224 C2H2-TYPE.
 FT ZN_FING 230 252 C2H2-TYPE.
 FT NON_TER 252 252
 SQ SEQUENCE 252 AA; 28872 MW; 13A72370B10F0BD7 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 252;
 Best Local Similarity 75.0%; Pred. No. 5.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
 Db 28 HTGEKPFT 35

Search completed: June 28, 2001, 15:54:40
 Job time: 128 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2001, 16:08:27 ; Search time 411.58 Seconds
(without alignments)
2.893 Million cell updates/sec

Title: US-09-724-406-32
Perfect score: 50
Sequence: 1 QHSGELPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	82.0	556	4 Q9UMP5	Q9ump5 homo sapien
2	40	80.0	488	10 Q9LGM4	Q9lgm4 oryza sativ
3	39	78.0	278	5 Q9V718	Q9v718 drosophila
4	39	78.0	405	4 Q9UFB7	Q9ufb7 homo sapien
5	39	78.0	571	4 Q9GZV8	Q9gzv8 homo sapien
6	39	78.0	594	5 Q20537	Q20537 caenorhabdi
7	39	78.0	606	4 Q9Y2D9	Q9y2d9 homo sapien
8	37	74.0	181	5 Q9W3J3	Q9w3j3 drosophila
9	37	74.0	384	2 Q46239	Q46239 clostridium
10	37	74.0	498	4 Q9H8L4	Q9h8l4 homo sapien
11	37	74.0	501	5 Q9VG72	Q9vg72 drosophila
12	37	74.0	525	5 Q9WN56	Q9wn56 drosophila
13	37	74.0	532	5 Q01960	Q01960 caenorhabdi
14	37	74.0	720	6 Q9N003	Q9n003 macaca fasc
15	37	74.0	756	5 Q61362	Q61362 drosophila
16	37	74.0	891	5 Q61361	Q61361 drosophila
17	37	74.0	934	5 Q9WKF1	Q9wkf1 drosophila
18	37	74.0	936	5 Q9VGK1	Q9vgk1 drosophila
19	37	74.0	962	5 Q61360	Q61360 drosophila

20	37	74.0	1143	10 Q92PS9	Q9zps9 arabidopsis
21	36	72.0	52	4 Q15923	Q15923 homo sapien
22	36	72.0	90	4 Q92669	Q92669 homo sapien
23	36	72.0	306	4 Q9NQJ3	Q9nqj3 homo sapien
24	36	72.0	349	2 Q9ZH35	Q9zh35 enterobacte
25	36	72.0	354	13 Q09047	Q09047 xenopus lae
26	36	72.0	382	5 Q9VP31	Q9vp31 drosophila
27	36	72.0	420	13 Q9PSM1	Q9psm1 xenopus lae
28	36	72.0	462	13 Q91906	Q91906 xenopus lae
29	36	72.0	478	4 Q9H5P0	Q9h5p0 homo sapien
30	36	72.0	484	4 Q13397	Q13397 homo sapien
31	36	72.0	493	13 Q08701	Q08701 xenopus lae
32	36	72.0	522	4 Q99592	Q99592 homo sapien
33	36	72.0	522	11 Q9WUK6	Q9wuk6 mus musculu
34	36	72.0	522	11 Q9JKY3	Q9jky3 rattus norv
35	36	72.0	547	4 Q9V5A5	Q9v5a5 homo sapien
36	36	72.0	549	5 Q9VE54	Q9ve54 drosophila
37	36	72.0	556	5 Q9VDN4	Q9vdn4 drosophila
38	36	72.0	556	5 Q9GRA5	Q9gra5 halocynthia
39	36	72.0	591	13 Q09046	Q09046 xenopus lae
40	36	72.0	634	4 Q9NSM4	Q9nsm4 homo sapien
41	36	72.0	648	4 Q9H1B9	Q9h1b9 homo sapien
42	36	72.0	692	4 Q9UJW8	Q9ujw8 homo sapien
43	36	72.0	692	4 Q9PLU2	Q9plu2 homo sapien
44	36	72.0	1001	4 Q9NAD7	Q9nxd7 homo sapien
45	36	72.0	1239	5 Q9VT48	Q9vt48 drosophila

ALIGNMENTS

RESULT 1
Q9UMP5
ID Q9UMP5 PRELIMINARY; PRT; 556 AA.
AC Q9UMP5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE AP4 PROTEIN.
GN AP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobner T.G., Fischer M., Groitl P.;
RT "Cloning of a novel zinc finger protein."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245553; CAB53100.1; -
DR HSSP; P08047; ISP2.
DR InterPro; IPR000822; -
DR Pfam; PF00096; zf-C2H2; 15.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 14.
DR SMART; SM00355; ZnF_C2H2; 1.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 556 AA; 62286 MW; E9CFFB4AF/CL2E90 CRC64;

Query Match 82.0%; Score 41; DB 4; Length 556;
Best Local Similarity 77.8%; Pred No. 4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
Db 385 QHTGERPFT 393
||:|:| |

RESULT 2
Q9LGM4 PRELIMINARY; PRT; 488 AA.
ID Q9LGM4
AC Q9LGM4;
DT 01-OCT-2000 (Tremblrel. 15, Created)

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DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ESTS AU075348(C11252).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
OC NCBI_TaxID=4530;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0041E11."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0433F09."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002521; BAA96760.1; -
DR EMBL; AP002539; BAB08199.1; -
DR InterPro; IPR001841; -
DR Pfam; PF00097; zf-C3HC4; 1.
SQ SEQUENCE 488 AA; 53169 MW; 1FBAD40A7463C373 CRC64;

Query Match 80.0%; Score 40; DB 10; Length 488;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSGELPPT 9
Db 235 HSGEMPPT 242

RESULT 3
Q9V718 ID Q9V718 PRELIMINARY; PRT; 278 AA.
AC Q9V718;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG17385 PROTEIN.
GN CG17385.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garb N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AF003814; AAF58248.1; -
DR HSSP; P08047; 1SP2
DR Flybase; FBgn0033934; CG17385.
DR InterPro; IPR000822; -
DR Pfam; PF00096; zf-C2H2; 7.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 7.
DR SMART; SM00355; ZnF_C2H2; 1.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 278 AA; 32463 MW; 3D6DE1AE5D77C223 CRC64;

Query Match 78.0%; Score 39; DB 5; Length 278;
Best Local Similarity 87.5%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGELPPT 9
Db 96 HSGERPPT 103

RESULT 4
Q9UF07 ID Q9UF07 PRELIMINARY; PRT; 405 AA.
AC Q9UF07;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN (FRAGMENT).
GN DKFZP343N0615.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AL133062; CAB61386.1; -
DR HSSP; P08047; 1SP2.
DR InterPro; IPR000822; -
DR Pfam; PF00096; zf-C2H2; 9.
DR PRINTS; PR00048; ZINC_FINGER.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 7.
DR SMART; SM00355; ZnF_C2H2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Zinc-finger.
FT NON-TER
SQ SEQUENCE 405 AA; 46007 MW; 72116A2A7ACDCB33 CRC64;

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Query Match 78.0% Score 39; DB 4; Length 405;
 Best Local Similarity 87.5%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPF 8
 |||||
 Db 227 QHSGEKPF 234

RESULT 5
 Q9GZV8 PRELIMINARY; PRT; 571 AA.
 AC Q9GZV8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE CONA FLJ12533 FIS, CLONE NT2RM4000202, WEAKLY SIMILAR TO ZINC FINGER
 GN PRDM14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takanashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Du Y., Yang X., Huang S.;
 RT "A family of novel PR-domain (PRDM) genes as candidate tumor
 RT suppressors.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK022595; BAB14120.1; -;
 DR EMBL; AF319458; AAG39635.1; -;
 SQ SEQUENCE 571 AA; 64062 MW; 60D5ACC96DADE500 CRC64;

Query Match 78.0% Score 39; DB 4; Length 571;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPF 8
 |||||
 Db 510 QHSGEKPF 517

RESULT 6
 Q20537 PRELIMINARY; PRT; 594 AA.
 AC Q20537;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE SIMILAR TO C2H2-TYPE ZINC FINGER.
 GN F47E1.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditida; Feloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lighning J., Loyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Favellio T.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL; U39993; AAA81086.1; -;
 DR HSP; P08046; 1A1H.
 DR InterPro: IPR000822; -;
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR PROSITE; PS00026; ZINC_FINGER_C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
 SQ SEQUENCE 594 AA; 67531 MW; 81957608C0CB5A7 CRC64;

Query Match 78.0% Score 39; DB 5; Length 594;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPF 8
 |||||
 Db 573 QHSGEKPF 580

RESULT 7
 Q9Y2D9 PRELIMINARY; PRT; 606 AA.
 ID Q9Y2D9;
 AC Q9Y2D9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE KIAA0924 PROTEIN.
 GN KIAA0924.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=BRAIN;
 RX MEDLINE=99246063; PubMed=10231032;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL; AB023141; BAA76768.1; -;
 DR HSP; P08047; 1SP2.
 DR InterPro: IPR000322; -;
 DR Pfam; PF00096; zf-C2H2; 9.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 7.

DR SMART; SM00355; Znf_C2H2; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
 SQ SEQUENCE 606 AA; 69744 MW; C066D10E179985CC CRC64;

Query Match 78.0%; Score 39; DB 4; Length 606;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPF 8
 :|||:|
 Db 378 QHSGEKP 385

RESULT 8
 Q9W3J3 PRELIMINARY; PRT; 181 AA.
 AC Q9W3J3
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CG15336 PROTEIN.
 GN CG15336.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Hejt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RL EMBL; AE003443; AAF4634.1;
 DR FlyBase; FBgn0030009; CG15336.
 DR InterPro; IPR000822; -

DR Pfam; PF00096; zf-C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 1.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 181 AA; 21222 MW; E6169EDF0025D605 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 181;
 Best Local Similarity 55.6%; Pred. No. 7.9;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QHSGELPF 9
 :|||:|
 Db 58 RUTGEMPF 66

RESULT 9
 Q46239 PRELIMINARY; PRT; 384 AA.
 AC Q46239;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE NANH GENE & ORF1,2,3 & 4 PRECURSOR.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A99;
 RX MEDLINE=95102306; PubMed=7804004;
 RA Traving C., Schauer R., Roggentin P.;
 RT "Gene structure of the 'large' sialidase isoenzyme from Clostridium
 perfringens A99 and its relationship with other clostridial nanH
 proteins.";
 RL Glycoconj. J. 11:141-151(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A99;
 RA Schauer R.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X87369; CAA60797.1; -;
 DR InterPro; IPR001798; -;
 DR Pfam; PF01344; Kelch; 2.
 KW Signal.
 FT SIGNAL. 1 19 POTENTIAL.
 FT CHAIN 20 384
 SQ SEQUENCE 384 AA; 42083 MW; E1E2589AFB1C6A9 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 384;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QHSGELPF 9
 :|||:|
 Db 157 KHIGDLPT 165

RESULT 10
 Q9H8L4 PRELIMINARY; PRT; 498 AA.
 AC Q9H8L4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CDNA FLJ13479 FIS, CLONE PLACE1003738, WEAKLY SIMILAR TO ZINC FINGER
 DE PROTEIN 135.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

[1]	SEQUENCE FROM N. A.
RR	TISSUE=PLACENTA;
RC	
RA	ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Sazuki Y.,
RA	Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA	Arinase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA	Tanaka M., Nabekura T., Ishii S., Kawai Y., Salco K., Yamamoto J.,
RA	Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Oshima A.;
RT	"NEO human CDNA sequencing project."
RT	Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
RL	EMBL; AK023541; BABI4602.1 ;
RS	SEQUENCE 498 AA; 54872 MW; C704FCF55CCDAE1A CRC64;
SD	

Query Match 74.0%; Score 37; DB 4; Length 498;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSGELPF 8
|:| | | |
Db 13 HAGELPF 19

RESULT	11
Q9VGV72	
ID	Q9VG72
AC	PRELIMINARY; PRT; 501 AA.
Q9VG72:	
01-MAY-2000	(TRENBLrel. 13, Created)
01-MAY-2000	(TRENBLrel. 13, Last sequence update)
01-MAR-2001	(TRENBLrel. 16, Last annotation update)
CG5245	PROTEIN.
CG5245:	
SUS	Drosophila melanogaster (Fruit fly).
CC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC	Ephydroidea; Drosophilidae; Drosophila.

SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amann T.S., Lewin S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Binkley S., Ward M.J., Zhou Y., Zheng X.,
Sutton G.G., Morten J.R., Mandel M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abul J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cuklew E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebj J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Purli V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of <i>Drosophila melanogaster</i> .";
RL	Science 287:2185-2195(2000).
RL	EMBL; AE003696; AAF54813.1; -.
DR	HSP: P08047; 1SP2.
DR	FlyBase; FBgn0038047; CG5245.
DR	InterPro; IPR000822; -.
DR	Pfam; PF00096; zf-C2H2; 15.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2; 14.
DR	SMART; SM00355; ZnF_C2H2; 1.
KW	DNA-binding; Metal-binding; Zinc-finger.
SQ	SEQUENCE 501 AA; 58790 MW; BBAE04740D41C43F CRC64;

Query Match	74.0%	Score 37;	DB 5;	Length 501;
Best Local Similarity	85.7%	Pred. No. 24;		
Matches	6; Conservative	1; Mismatches	0; Indels	

QY 2 HSGELPF 8
Db 438 HTGELPF 444

RESULT	12	
Q9VN56		
ID	Q9VN56	PRELIMINARY; PRT; 525 AA.
AC	Q9VN56;	
DT	01-MAY-2000	(T=EMBLrel. 13, Created)
DT	01-MAY-2000	(T=EMBLrel. 13, Last sequence update)
DT	01-MAR-2001	(T=EMBLrel. 16, Last annotation update)
DE	CG14655	PROTEIN.
DE	CG14655.	
GN	Drosophila	melanogaster (Fruit fly).
OS	Drosophila	melanogaster (Fruit fly).
OC	Eukaryota;	Metazoa; Arthropoda; Tracheata; Insecta;
OC	Pterygota;	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea;	Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;	
RN	[1]	

SEQUENCE FROM N.A.
STRAIN-BERKELEY.
MEDLINE-19731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Mortman J.R., Wandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow R.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Bereman B.P., Shandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Duqan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobbarr C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003605; AAF52094.1; -;
DR HSSP; P07248; IPAA.
DR FlyBase; FBgn0037275; CG14655.
DR InterPro; IPR000822; -;
DR Pfam; PF00096; zf-C2H2; 7.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 7.
DR SMART; SM00355; ZnF_C2H2; 1.
DR DNA-binding; Metal-binding; Zinc-finger.
KW SEQUENCE 525 AA; 58076 MW; 69DEIAE3CA739727 CRC64;
SQ

Query Match 74.0%; Score 37; DB 5; Length 525;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 HSGELPFT 9
|:|:|:|:
Db 288 HTGEMPT 295

RESULT 13
O01960 PRELIMINARY; PRT; 532 AA.
AC O01960;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE SIMILARITY TO MULTIPLE C2H2-TYPE ZINC FINGERS.
GN C27A12.3.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Murray J., Wohlmann P., Blewald T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AF003137; AAB93641.1; -;
DR HSSP; P07248; 2ADR.
DR InterPro; IPR000822; -;
DR Pfam; PF00096; zf-C2H2; 6.
DR PRINTS; PR00048; ZINC_FINGER.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; UNKNOWN_6.
DR SMART; SM00355; ZnF_C2H2; 1.
DR DNA-binding; Nuclear protein; Zinc-finger.
KW SEQUENCE 532 AA; 61223 MW; 154682344C6D2E4E CRC64;
SQ

Query Match 74.0%; Score 37; DB 5; Length 532;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 8
|:|:|:|:
Db 113 QHMGDLPT 120

RESULT 14
Q9N003 PRELIMINARY; PRT; 720 AA.
AC Q9N003;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE HYPOTHETICAL 83.9 KDA PROTEIN.
OS *Macaca fascicularis* (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM CORTEX;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046644; BAB03562.1; -;
DR InterPro; IPR000822; -;
DR InterPro; IPR001909; -;
DR Pfam; PF00096; zf-C2H2; 19.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 19.
DR SMART; SM00349; KRAB; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Zinc-finger.
SQ SEQUENCE 720 AA; 83922 MW; 074A7736A5903D90 CRC64;
SQ

Query Match 74.0%; Score 37; DB 6; Length 720;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPFT 9
|:|:|:|:
Db 599 QHSGQKFFS 607

RESULT 15
O61362 PRELIMINARY; PRT; 756 AA.
AC O61362;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CROL GAMMA.
GN CROL OR CROL GAMMA OR CG14938.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_taxid=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA D'Avino P.P., Thummel C.S.;
 RL Submitted (JUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 DR EMBL; AF020349; AAC15518.1; -.
 DR HSP; P08047; ISP2.
 DR FlyBase; FBgn0020309; crol.
 DR InterPro; IPR000822; -.
 DR Pfam; PF00096; zf-C2H2; 12.
 DR PRINTS; PR00048; ZINC_FINGER.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2; 12.
 DR SMART; SM00355; ZnF_C2H2; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
 SQ SEQUENCE 756 AA; 82883 MW; FA5DF25B09E74642 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 756;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHSGELPF 8
 Db 288 QHTGETPF 295

Search completed: June 28, 2001, 16:08:28
 Job time: 956 sec

